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(21) International Application Number: PCT/US93/03615 (22) International Filing Date: 13 April 1993 (13.04.93) (30) Priority data: 868,596 14 April 1992 (14.04.92) US (60) Parent Application or Grant (63) Related by Continuation US 868,596 (CIP) Filed on 14 April 1992 (14.04.92) (71) Applicant (for all designated States except US): THE MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY UNIVERSITY OF NEW YORK [US/US]; One Gustave Levy Place, New York, NY 10029 (US).		(72) Inventor; and (75) Inventor/Applicant (for US only) : PALESE, Peter [US/US]; 414 Highwood Avenue, Leonia, NJ 07605 (US). (74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US). (81) Designated States: AU, BB, BG, BR, CA, CZ, FI, GB, HU, JP, KR, KZ, LK, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>
(54) Title: GENETICALLY ENGINEERED ATTENUATED VIRUSES (57) Abstract The present invention relates to engineering attenuated viruses by altering a non-coding region or the coding sequence of a viral gene. Alterations of the non-coding regions which regulate transcription and/or replication are described. These alterations result in the down-regulation of the viral gene and an attenuation of the virus, either by the production of defective particles during replication, or by reducing the number of progeny virions produced during viral replication. Alterations of viral coding sequences are also described which result in a recombinant or chimeric attenuated virus.		

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GENETICALLY ENGINEERED ATTENUATED VIRUSES

This is a Continuation-In-Part of Serial No.
07/868,596 filed April 14, 1992, which is incorporated
5 by reference herein in its entirety.

The work reflected in this application was
supported, in part, by a grant from the National
Institutes of Health, and the Government may have
10 certain rights in the invention.

1. INTRODUCTION

The present invention relates to engineering
attenuated viruses by altering a non-coding region or
15 the coding sequence of a viral gene. Alterations of
the non-coding regions which regulate transcription
and/or replication are described. These alterations
result in the down-regulation of the viral gene and an
attenuation of the virus, either by the production of
20 defective particles during replication, or by reducing
the number of progeny virions produced during viral
replication. Alterations of viral coding sequences
are also described which result in a recombinant or
chimeric attenuated virus.

25

2. BACKGROUND OF THE INVENTION

Inactivated virus vaccines are prepared by
"killing" the viral pathogen, e.g., by heat or
formalin treatment, so that it is not capable of
30 replication. Inactivated vaccines have limited
utility because they do not provide long lasting
immunity and, therefore, afford limited protection.
An alternative approach for producing virus vaccines
involves the use of attenuated live virus vaccines.
35 Attenuated viruses are capable of replication but are
not pathogenic, and, therefore, provide for long r
lasting immunity and afford greater protection.

However, the conventional methods for producing attenuated viruses involve the chance isolation of host range mutants, many of which are temperature sensitive; e.g., the virus is passaged through
5 unnatural hosts, and progeny viruses which are immunogenic, yet not pathogenic, are selected.

Recombinant DNA technology and genetic engineering techniques, in theory, would afford a superior approach to producing an attenuated virus
10 since specific mutations could be deliberately engineered into the viral genome. However, the genetic alterations required for attenuation of viruses are not known or predictable. In general, the attempts to use recombinant DNA technology to engineer
15 viral vaccines have mostly been directed to the production of subunit vaccines which contain only the protein subunits of the pathogen involved in the immune response, expressed in recombinant viral vectors such as vaccinia virus or baculovirus. More
20 recently, recombinant DNA techniques have been utilized in an attempt to produce herpes virus deletion mutants or polioviruses which mimic attenuated viruses found in nature or known host range mutants. Until very recently, the negative strand RNA
25 viruses were not amenable to site-specific manipulation at all, and thus could not be genetically engineered.

3. SUMMARY OF THE INVENTION

30 The present invention relates to the production of attenuated viruses using recombinant DNA techniques. At least two approaches for engineering attenuated viruses are described. One approach involves engineering alterations of a non-coding
35 region of the virus that regulates transcription and/or replication of a viral gene so that at least one of the viral genes is down regulated. This

approach may be applied to a number of different viruses and is advantageously used to engineer segmented viruses where down regulation of the synthesis of one viral segment results in the
5 generation of defective particles during each round of viral replication so that the progeny viruses demonstrate attenuated characteristics. In non-segmented viruses, the down regulation of a viral gene can result in a decrease in the number of infectious
10 virions produced during replication, so that the virus demonstrates attenuated characteristics.

A second approach involves engineering alterations of a viral coding region so that the viral protein expressed is altered by the insertion,
15 deletion or substitution of an amino acid residue or an epitope and an attenuated chimeric virus is produced.

The attenuated viruses of the invention may advantageously be used safely in live virus vaccine
20 formulation. As used herein, the term "attenuated" virus refers to a virus which is infectious but not pathogenic; or an infectious virus which may or may not be pathogenic, but which either produces defective particles during each round of replication or produces
25 fewer progeny virions than does the corresponding wild type virus during replication. Pathogenic viruses which are engineered to produce defective particles or a reduced number of progeny virions are "attenuated" in that even though the virus is capable of causing
30 disease, the titers of virus obtained in a vaccinated individual will provide only subclinical levels of infection.

4. DESCRIPTION OF THE FIGURES

35 FIG. 1. The noncoding sequences of the NA segments of influenza A/WSN/33 virus and of the NA/B-NS transfectant virus. The 5'- and 3'-terminal

sequences are drawn in a panhandle structure, which consists of two base-paired stems and one mismatched internal-loop in the middle. The noncoding nucleotides of the chimeric NA gene of the NA/B-NS virus are derived from the NS gene of influenza B/Lee virus. The large letters indicate nucleotides in the 5' and 3' terminal regions (containing 13 and 12 nucleotides, respectively) which are different for the two NA genes. The panhandle structure of the wild type virus NA gene is divided into regions A/D, B/E, and C/F, and that of the attenuated gene into a/d, b/e, and c/f. Regions B/E and b/e contain the second stem regions of the NA and the NA/B-NS genes, respectively. The open triangle marks the altered Kozak sequence in the NA gene of the NA/B-NS virus.

FIG. 2. Characterization of the RNA of the NA/B-NS virus. A. RNA electrophoresis. The RNAs extracted from purified viruses were analyzed on a 3% polyacrylamide gel containing 7.7 M urea and visualized by silver staining. Lane 1, RNA of influenza A WSN/33 virus; lane 2, RNA of NA/B-NS transfectant virus; lane 3, RNA obtained by run-off transcription from plasmid Pt_{NA/B-NS} which produces the chimeric NA RNA. B. Analysis of NA RNA in virions by ribonuclease protection assay (RPA). 50 ng of RNA extracted from purified virus was used in the hybridization reaction with positive sense NS and NA specific riboprobes as described in Materials and Methods. The protected probes were electrophoresed on a 6% acrylamide gel containing 7 M urea. Lane 1: riboprobes without RNase A/T₁ digestion; lane 2: riboprobes following RNase A/T₁ digestion; lane 3: riboprobes protected by the RNA of influenza A/WSN/33 virus; and lane 4: riboprobes protected by the RNA of NA/B-NS transfectant virus. C. Quantitation of NA-specific RNA in virus by primer extension. The vRNA extracted from either WSN/33 virus (lane 2) or NA/B-NS

transfectant virus (lane 3) was reverse transcribed by
Rnase H minus reverse transcriptase using NS and NA
segment specific primers as described in Materials and
Methods. The products for the NS RNAs are 195 nt long
5 and those for the NA RNAs approximately 260 nt long.
The products were analyzed on a 6% polyacrylamide gel
containing 7M urea. Size markers are shown on the
left.

FIG. 3. Time course of mRNA synthesis in MDBK
10 cells. A. Quantitation of NA- and NS-specific mRNAs
at different times p.i. by ribonuclease protection
assay (RPA). The diagram on the top schematically
illustrates the procedure. Both NS and NA probes are
minus sense, and contain sequences corresponding to
15 the 3'-terminal side of the cRNA, flanked by vector
sequences at the 3'-terminus as indicated by the open
rectangles. The sizes of the probes are shown on the
top, and the sizes of the resulting products are
indicated at the bottom of the diagram. The time
20 points (hrs) are indicated on the top. The positions
of probes and products on the gel are indicated by
arrows at the left and right, respectively. B. Time
course of NS-specific mRNA synthesis. The amount of
the NS mRNA was measured by direct counting the
25 radioactivity (counts per minute) in the corresponding
band excised from the gel shown in panel A. C.
Comparison of NA-specific mRNA synthesis of
transfectant virus and A/WSN/33 virus in infected
cells. The amount of mRNA for each time point was
30 determined as described in panel B.

FIG. 4. Analysis of NA-specific vRNA synthesis
in infected cells by primer extension. RNA isolated
from infected cells was reverse transcribed using
reverse transcriptase and NA and NS vRNA-specific
35 primers, as described in Materials and Methods. vRNAs
extracted from purified virus were used as control
(right). The resulting products were displayed on a

6% acrylamide denaturing gel. The reverse transcripts of the NS RNAs are 195 nt long and those of the NA-specific segments are approximately 260 nt long, as indicated by arrows at the right. The numbers on the top indicate the times (hrs) postinfection. Virion represents the RNA obtained from purified virus.

FIG. 5. Analysis of NA protein in virion and in infected cells. A. Western analysis of NA protein in virion. As described in Materials and Methods, a monoclonal antibody directed against carbohydrate was used to quantitate the glycoprotein in the viruses. The proteins are indicated by HA0 (uncleaved HA), HA1 (subunit 1 of HA) AND NA at the right. B. Viral proteins synthesized in infected cells. At different times postinfection (hrs p.i.), the viral proteins were labelled with ^{35}S [cysteine] for 30 minutes, and analyzed on a 10% Laemmli gel. The different proteins are marked at the right. The position of the NA protein is indicated by an arrow. The amount of NA protein was determined by counting the gel a radioanalytic AMBIS imaging system using NP and M1 proteins as controls.

FIG. 6. Vector for construction of chimeric HA molecules. FIG. 6A. Chimeric HA/ME1 malaria construct. FIG. 6B. Chimeric HA/polio VP1 construct.

FIG. 7. Schematic Structure of Neuraminidase (NA). Tetrameric NA inserted in viral membrane is depicted. Ct, cytoplasmic tail; TM, transmembrane domain; Stalk, stalk region; Head, the globular domain most distal to the viral membrane.

FIG. 8. Diagram of neuraminidase mutants. The four domains of the neuraminidase molecule are indicated: CT, cytoplasmic tail; TM, transmembrane domain; Stalk, stalk region and Head, the globular domain most distal to the viral membrane. The numbering system of the amino acids is according to Hiti and Nayak, 1982, J. Virol. 41:730-734. Deletions

ar as indicated, and insertions and mutations in the stalk region are underlined. The diagram is not drawn to scale. (+) indicates that infectious virus was rescued following transfection of the mutant RNA.

5 FIG. 9. Gel analysis of vRNAs extracted from purified viruses. Viruses and vRNAs were prepared as described in Section 9.1. 200 ng virion RNA was analyzed on a 2.8% polyacrylamide gel containing 7.7 M urea. The RNA segments were visualized by silver
10 staining as described previously (Enami et al., 1990, Proc. Natl. Acad. Sci. USA 87:3802-3805). Each RNA segment is indicated at the left. Lane 1, wild type transfected virus. Lane 2, Del 16 mutant virus. Lane 3, Ins 12 mutant virus. Lane 4, Ins 24 mutant virus.
15 Lane 5, Ins 41 mutant virus. Arrows indicate the position of the NA genes in each of the RNA preparations.

FIG. 10. Analysis of vRNA by reverse transcription and PCR. RNA extracted from purified
20 virus was reverse transcribed and the NA gene-specific transcripts were then amplified by PCR as described in Section 9.1. The PCR products labelled with gamma [³²P] ATP were analyzed on a 6% polyacrylamide gel containing 7 M urea (Luo et al., 1991, J. Virol.
25 65:2861-2867). The expected products for wild type NA, Del 18m, Del 23N and Del 28N mutant NAs were 214, 160, 145 and 130 nucleotides long, respectively. PhiX174 RF DNA/Hae III fragments (BRL, Bethesda, MD) were labelled with gamma ³²[P]ATP and were used as size
30 markers. The sizes of the DNA fragments are indicated at the left. Lane 1, size marker. Lane 2, product of wild type NA (T3NAMod). Lane 3, product of Del 18m mutant NA. Lane 4, product of Del 23N mutant NA. Lane 5, product of Del 28N mutant NA. Arrows
35 indicated the position of the PCR products.

FIG. 11. Growth curves of transfectant viruses in MDBK (A.) and MDCK (B.) cells. Cells were infected

with wild type or mutant viruses at the m.o.i. of 0.001 and virus titers of supernatant collected at the indicated times were determined as described in Section 9.1.

5

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to genetically engineered attenuated viruses, and methods for their production. Recombinant DNA techniques can be
10 utilized to engineer site specific mutations into one or more noncoding regions of the viral genome which result in the down-regulation of one or more viral genes. Alternatively, recombinant DNA techniques can be used to engineer a mutation, including but not
15 limited to an insertion, deletion, or substitution of an amino acid residue(s) or an epitope(s) into a coding region of the viral genome so that altered or chimeric viral proteins are expressed by the engineered virus. The invention is based, in part, on
20 the discovery that the down regulation of a viral gene in segmented viruses results in the production of defective particles at each round of replication, so that the virus demonstrates attenuated characteristics. In non-segmented viruses, the down-
25 regulation of a viral gene may result in the production of fewer progeny virions than would be generated by the corresponding wild type virus. The alterations of the viral proteins described also result in attenuation for reasons which are less well
30 understood.

Many methods may be used to introduce the live attenuated virus formulations to a human or animal subject to induce an immune response; these include, but are not limited to, oral, intradermal,
35 intramuscular, intraperitoneal, intravenous, subcutaneous and intranasal routes. It is preferable

to introduce the chimeric virus vaccine via its natural route of infection.

Any virus may be engineered in accordance with the invention to produce an attenuated strain suitable for use as a safe live-virus vaccine, including but not limited to viruses belonging to the families set forth in Table I below.

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TABLE I
FAMILIES OF HUMAN AND ANIMAL VIRUSES

5	<u>VIRUS CHARACTERISTICS</u>	<u>VIRUS FAMILY</u>
	dsDNA	
	Enveloped	Poxviridae Irididoviridae Herpesviridae
10	Nonenveloped	Adenoviridae Papovaviridae Hepadnaviridae
	ssDNA	
	Nonenveloped	Parvoviridae
15	dsRNA	
	Nonenveloped	Reoviridae Birnaviridae
	ssRNA	
	Enveloped	
	Positive-Sense Genome	
	No DNA Step in Replication	Togaviridae Flaviviridae Coronaviridae Hepatitis C Virus
20		
	DNA Step in Replication	Retroviridae
	Negative-Sense Genome	
	Non-Segmented Genome	Paramyxoviridae Rhabdoviridae Filoviridae
25		
	Segmented Genome	Orthomyxoviridae Bunyaviridae Arenaviridae
30	Nonenveloped	Picornaviridae Calciviridae

Abbreviations used: ds = double stranded; ss = single stranded; enveloped = possessing an outer lipid bilayer derived from the host cell membrane; positive-sense genome = for RNA viruses, genomes that are composed of nucleotide sequences that are directly translated on ribosomes; = for DNA viruses, genomes that are composed of nucleotide sequences that are the same as the mRNA; negative-sense genome = genomes that are composed of nucleotide sequences complementary to the positive-sense strand.

DNA viruses (e.g., vaccinia, adenoviruses, baculovirus) and positive strand RNA viruses (e.g., poliovirus) may be readily engineered using recombinant DNA techniques which are well known in the art (e.g., see U.S. Patent No. 4,769,330 to Paoletti; U.S. Patent No. 4,215,051 to Smith; Racaniello et al., 1981, Science 214: 916-919). Until recently, however, negative strand RNA viruses (e.g., influenza) were not amenable to site specific genetic manipulation because the viral RNAs are not infectious. However, a recently developed technique, called "reverse genetics," allows the engineering and production of recombinant negative strand RNA viruses.

The reverse genetics technique involves the preparation of synthetic recombinant viral RNAs that contain the non-coding regions of the negative strand virus which are essential for the recognition of viral RNA by viral polymerases and for packaging signals necessary to generate a mature virion. The recombinant RNAs are synthesized from a recombinant DNA template and reconstituted in vitro with purified viral polymerase complex to form recombinant ribonucleoproteins (RNPs) which can be used to transfect cells. A more efficient transfection is achieved if the viral polymerase proteins are present during in vitro transcription of the synthetic RNAs. The synthetic recombinant RNPs can be rescued into infectious virus particles. The foregoing techniques are described in copending application Serial No. 07/527,237 filed May 22, 1990 and in Enami & Palese, 1991, J. Virol. 65: 2711-2713, each of which is incorporated by reference herein in its entirety), and influenza A viruses containing insertions, deletions and mutations with the stalk portion of the NA gene, one of which changes acts as a host range mutant. Using the reverse genetics technique, the following recombinant negative-strand viruses were engineered:

an influenza virus containing nine different RNA segments; a chimeric influenza A virus (NA/B-NS) in which the noncoding region of the NA gene was replaced by that belonging to an influenza B virus NS gene; an influenza A virus with chimeric hemagglutinins containing epitopes from different influenza subtypes (Enami et al., 1991, Virology 185: 291-298; Muster et al., 1991, Proc. Natl. Acad. Sci. USA 88: 5711-5781; copending application Serial No. 07/841,310 filed February 3, 1992; and Li et al., 1992, J. Virol. 66: 399-404; each of which is incorporated by reference herein in its entirety); and influenza A viruses containing insertions, deletions, and mutations within the stalk portion of the NA gene, one of which acts as a host range mutant. The invention is discussed in more detail in the subsections below and the examples infra. For clarity, the details of the invention are described using influenza. However, the principles may be analogously applied to construct other attenuated viruses.

5.1. DOWN-REGULATION OF VIRAL GENES

In accordance with the invention, a non-coding regulatory region of a virus can be altered to down-regulate any viral gene, e.g. reduce transcription of its mRNA and/or reduce replication of vRNA (viral RNA), so that an attenuated virus is produced.

This approach, while applicable to any virus, is particularly attractive for engineering viruses with segmented genomes; i.e., viruses in which the genome is divided into segments that are packaged into virions. For example, the segmented genome of influenza A virus (an orthomyxovirus) consists of eight molecules of linear negative-sense ssRNAs which ncode ten polypeptides, including: the RNA-directed RNA polymerase proteins (PB2, PB1 and PA) and nucleoprotein (NP) which form the nucleocapsid; two

surface glycoproteins which project from the envelope: hemagglutinin (HA) and neuraminidase (NA); and nonstructural proteins (NS1 and NS2) whose function is unknown. The termini of each segment contain the non-coding regions essential for recognition by viral polymerase and for packaging signals necessary to generate a mature virion. The sequence of the termini is highly conserved among all eight segments. As another example, the segmented genome of reoviruses consists of 10 to 12 segments of linear dsRNA which encode 6 to 10 major structural polypeptides, a transcriptase and other enzymes.

Alterations of non-coding regulatory regions of segmented viruses which result in down-regulation of replication of a viral gene segment, and/or down-regulation of transcription of a viral gene will result in the production of defective particles in each round of replication; i.e. particles which package less than the full complement of viral segments required for a fully infectious, pathogenic virus. Therefore, the altered virus will demonstrate attenuated characteristics in that the virus will shed more defective particles than wild type particles in each round of replication. However, since the amount of protein synthesized in each round is similar for both wild type virus and the defective particles, such attenuated viruses are capable of inducing a good immune response.

The foregoing approach is equally applicable to non-segmented viruses, where the down regulation of transcription of a viral gene will reduce the production of its mRNA and the encoded gene product. Where the viral gene encodes a structural protein, e.g., a capsid, matrix, surface or envelope protein, the number of particles produced during replication will be reduced so that the altered virus demonstrates attenuated characteristics; e.g., a titer which

results in subclinical levels of infection. For example, a decrease in viral capsid expression will reduce the number of nucleocapsids packaged during replication, whereas a decrease in expression of the envelope protein may reduce the number and/or infectivity of progeny virions. Alternatively, a decrease in expression of the viral enzymes required for replication, e.g., the polymerase, replicase, helicase, and the like, should decrease the number of progeny genomes generated during replication. Since the number of infectious particles produced during replication are reduced, the altered viruses demonstrate attenuated characteristics. However, the number of antigenic virus particles produced will be sufficient to induce a vigorous immune response.

Any alteration of the regulatory non-coding regions which decrease their efficiency or strength may be engineered in accordance in the invention. For example, the strength of viral promoters can be reduced by alterations in the stem structure. In the experiments detailed herein, specific nucleotide changes in the second stem structure of the promoter (B/E in FIG. 1) at the termini of the vRNAs which make up the panhandle structure of segmented negative-strand RNA viruses, such as influenza, were found to be responsible for the down-regulation of the synthesis of one vRNA segment. In particular, the UCCU/AGGA nucleotides of the chimeric influenza mutant NA/DeF/AbC (Section 7.2.1, Table III) are the critical base pairs involved. (The comparable base pairs in the wild type are CUC/GAG).

This base pair combination was introduced into the non-coding regulatory regions for other viral genes. Results indicate that the chimeric viruses so produced are also attenuated. Apparently, changes in this second stem structure lead to a reduction in vRNA synthesis of the viral segment, which is accompanied

by a reduction in the number of infectious particles containing a full complement of all eight RNA segments. It should also be noted that the reversion rate of the changed stem structure is extremely low, since reversion would require the simultaneous change of two nucleotides.

While the engineered reduction in vRNA or mRNA produces attenuation, this is not accompanied by a significant reduction in the viral protein specified by the gene. In fact, it may be desirable to engineer strong translation signals into the viral gene so that the gene transcripts which are present at low concentrations are efficiently translated into viral proteins required to provide some degree of replication.

The experiments described in the examples detailed infra were designed to understand the molecular mechanism underlying the changed growth characteristics of the chimeric NA/B-NS virus, as well as other engineered viruses described herein (e.g., RAM 3, HA/malaria ME 1, and HA/poliovirus 1) with the aim of developing a prototype for live virus vaccines. The NA/B-NS is a transfectant influenza A virus containing a chimeric NA gene in which the noncoding sequences are identical to those in the NS gene of influenza B/Lee virus described in copending application Serial No. 07/841,310, filed February 3, 1992 by Palese et al.; and in Muster et al., 1991, Proc. Natl. Acad. Sci. USA 88: 5177-5181 each of which is incorporated by reference herein in its entirety). This virus has many unique growth characteristics in tissue culture and it is highly attenuated in mice.

Several lines of evidence obtained from the experiments described herein indicate that the cis elements derived from the influenza B/Lee virus gene are responsible for the dramatic effects on transcription and replication of the chimeric NA gene

of the NA/B-NS transfectant virus. It was found that the NA gene had a six-fold lower representation in the purified viral preparation than did the remaining seven RNAs (see Sections 6.2.2 and 6.2.4, infra).

5 This strikingly lower representation of one RNA is compatible with the finding that the NA/B-NS transfectant virus has an approximately 5- to 10-fold lower infectious particle to physical particle ratio than wild type virus (see Section 6.2.1, infra). It
10 is assumed that an infectious virus would require the presence of a full complement of all eight influenza virus RNA segments. Many of the NA/B-NS progeny virus, however, lack an NA gene, so that more defective particles are formed than is the case in a
15 wild type virus infection. It is not clear whether this 5- to 10-fold reduction in titer is only the reflection of the lower representation of the NA gene or whether other factors also play a role. For example, some viruses may contain defective
20 interfering RNAs which would lower the infectivity titer of the preparation.

The mRNA synthesis of the NA is also considerably reduced in transfectant virus-infected cells (see Section 6.2.4, infra). Surprisingly, this does not
25 lead to a commensurate reduction in protein synthesis. Both virus-infected cells and purified virus show only a two-fold lower level of NA protein relative to that of wild type-infected cells or of purified wild type virus itself (see Section 6.2.3, infra). This higher
30 than expected level of NA protein in the transfectant virus may be the result of a good Kozak sequence present in the chimeric NA gene. The chimeric NA gene has an A in the -3 position instead of the U found in the wild type NA RNA (see open triangle in FIG. 1).
35 The data also indicate that the two-fold reduction in NA activity does not significantly influence the pathogenicity of the virus, since other transfectant

viruses were constructed (e.g., NAM 3 shown below) in which the expression of the NA gene is down regulated by a factor of 10 without affecting virus growth in tissue culture (see Section 7.2.2 and Table IV,

5 infra):

```

      AG.A      A      UUUGAACAAACAUI
AGU    AAC.. AGGAGUUU
UCG    UUG    UCCUCAAA
      ...U    CG      CUUAC

```

It should be noted that in the transfectant
 10 virus, expression of the other seven genes is not altered. Specifically, the NA/B-NS virus produces the same level of HA protein as found in wild type virus and comparable amounts of HA are packaged into the envelope of the virus. It appears that the
 15 attenuation characteristic is best explained by the lower synthesis of NA-specific vRNA and by the resulting lower representation of particles containing a full complement of the eight RNA segments.

How influenza A virus packages its eight RNA
 20 genome segments remains an interesting question. In the past, two different mechanisms were proposed for the packaging of influenza virus RNAs: one suggests that the eight RNAs are selectively packaged and the other that viral RNAs are packaged randomly (Compans
 25 et al., 1970, In The Biology Of Large RNA Viruses, Barry & Mahy, Eds., pp. 87-108, Academic Press, N.Y.; Lamb & Choppin, 1983, Ann. Rev. Biochem. 467-506; Smith & Hay, 1982, Virology 118: 96-108). Evidence is now accumulating to support the random packaging
 30 mechanism. The random packaging theory originated from the fact that influenza viruses have a low ratio of infectious particles to physical particles. If one assumes that an average of 11 RNAs are packaged per virion, the expected ratio is compatible with that
 35 found in vivo (Enami et al., 1991, Virology 185: 291-298). This model was also supported by the finding of a reassortant virus which contained two copies of the

same segment derived from two different viruses (Scholtissek, 1978, Virology 89: 506-516), and further support for this theory can come from a more recent report which described an influenza A virus which required
5 nine RNAs in order to be infectious (Enami et al., 1991, Virology 185: 291-298). The data described in the examples, infra, concerning the characterization of the NA/B-NS transfectant virus also seem to favor the random packaging mechanism rather than the
10 selective one. The lower level of chimeric NA RNA found in virions is consistent with the reduction of its synthesis in infected cells. In a selective packaging model, it would be expected that approximately equimolar amounts of chimeric NA RNA
15 would be packaged into virus particles.

In summary, the experiments described infra, indicate that influenza viruses for which the synthesis of a vRNA segment is down-regulated produce defective particles during replication. Since the
20 proteins of this virus are unaltered as compared to wild type virus, attenuation must be the result of inefficient cis-acting signals. This principle of attenuation may be applied analogously to other viruses with segmented genomes. For example, the
25 introduction of modifications into the noncoding sequences of rotavirus genes or of genes of other segmented dsRNA viruses (Roner et al., 1990, Virology 179: 845-852) should also allow the pathogenicity of these viruses to be altered.

30

5.2. ALTERATION OF VIRAL PROTEINS

An alternative way to engineer attenuated viruses involves the introduction of an alteration, including but not limited to an insertion, deletion or
35 substitution of one or more amino acid residues and/or epitopes into one or more of the viral proteins. This may be readily accomplished by engineering the

appropriate alteration into the corresponding viral gene sequence. Any change that alters the activity of the viral protein so that viral replication is modified or reduced may be accomplished in accordance
5 with the invention.

For example, alterations that interfere with but do not completely abolish viral attachment to host cell receptors and ensuing infection can be engineered into viral surface antigens or viral proteases
10 involved in processing to produce an attenuated strain. According to this embodiment, viral surface antigens can be modified to contain insertions, substitution or deletions of one or more amino acids or epitopes that interfere with or reduce the binding
15 affinity of the viral antigen for the host cell receptors. This approach offers an added advantage in that a chimeric virus which expresses a foreign epitope may be produced which also demonstrates attenuated characteristics. Such viruses are ideal
20 candidates for use as live recombinant vaccines. For example, heterologous gene sequences that can be engineered into the chimeric viruses of the invention include, but are not limited to, epitopes of human immunodeficiency virus (HIV) such as gp120; hepatitis
25 B virus surface antigen (HBsAg); the glycoproteins of herpes virus (e.g., gD, gE); VP1 of poliovirus; and antigenic determinants of nonviral pathogens such as bacteria and parasites to name but a few.

In this regard, influenza is an ideal system in
30 which to engineer foreign epitopes, because the ability to select from thousands of influenza virus variants for constructing chimeric viruses obviates the problem of host resistance or immune tolerance encountered when using other virus vectors such as
35 vaccinia. In addition, since influenza stimulates a vigorous secretory and cytotoxic T cell response, the presentation of foreign epitopes in the influenza

background may also provide for the secretory immunity and cell-mediated immunity. By way of example, the insertion, deletion or substitution of amino acid residues in the HA protein of influenza can be engineered to produce an attenuated strain. In this regard, alterations to the B region or E region of HA may be utilized. In accordance with this approach, the malarial epitope (ME 1) of Plasmodium yoelii (NEDSYVPSAEQI) was introduced into the antigenic site E of the hemagglutinin of influenza. The resulting chimeric virus has a 500- to 1,000-fold lower LD₅₀ (lethal dose 50) than that of wild type virus when assayed in mice. In another embodiment, the major antigenic determinant of poliovirus type 1, i.e., the BC loop of the VP1 of poliovirus type 1 (PASTTNKDKL) was engineered into the B region of the influenza HA protein. This chimeric virus is also attenuated (e.g., see Section 8, infra).

In another embodiment, alterations of viral proteases required for processing viral proteins can be engineered to produce attenuation. Alterations which affect enzyme activity and render the enzyme less efficient in processing, should affect viral infectivity, packaging, and/or release to produce an attenuated virus. For example, alterations to the NA protein of influenza can be engineered to reduce NA enzyme activity and decrease the number and/or infectivity of progeny virus released during replication. The example presented in Section 9 describes the production of an influenza A recombinant virus containing a deletion in the stalk region of the NA gene. This mutant acts as a host range mutant, i.e., a virus that has lost the capability to infect certain cell types. In another example, the protease of togaviruses, flaviviruses or hepatitis C virus (HCV) could be altered so that appropriate cleavage of the viral polyprotein is reduced, resulting in a

decrease in the number of progeny virions produced during replication.

In another embodiment, viral enzymes involved in viral replication and transcription of viral genes, 5 e.g., viral polymerases, replicases, helicases, etc. may be altered so that the enzyme is less efficient or active. Reduction in such enzyme activity may result in the production of fewer progeny genomes and/or viral transcripts so that fewer infectious particles 10 are produced during replication.

The alterations engineered into any of the viral enzymes include but are not limited to insertions, deletions and substitutions in the amino acid sequence of the active site of the molecule. For example, the 15 binding site of the enzyme could be altered so that its binding affinity for substrate is reduced, and as a result, the enzyme is less specific and/or efficient. For example, a target of choice is the viral polymerase complex since temperature sensitive 20 mutations exist in all polymerase proteins. Thus, changes introduced into the amino acid positions associated with such temperature sensitivity can be engineered into the viral polymerase gene so that an attenuated strain is produced.

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6. EXAMPLE: REDUCED TRANSCRIPTION AND
REPLICATION OF NA GENE OF INFLUENZA
NA/B-NS IS RESPONSIBLE FOR ATTENUATION

In order to understand the molecular characteristics responsible for the attenuation of the 30 transfectant virus, NA/B-NS, the following series of experiments were carried out to analyze the virus at the molecular level. The data presented in the subsections below indicate that attenuation results from the effect of the altered cis elements on the 35 replication of the chimeric NA gene. A low level of the NA gene in the virus preparation results in a

higher proportion of defective particles than is found in wild type virus preparation. In addition, the data support a random mechanism for the packaging of vRNAs into influenza virus particles.

5

6.1. MATERIALS AND METHODS

6.1.1. VIRUSES AND CELLS

The stocks of influenza A/WSN/33 virus and NA/B-NS transfectant virus (Muster et al., 1991, Proc.

10 Natl. Acad. Sci. USA 88: 5177-5181) were prepared from purified plaques by growing them in Madin-Darby bovine kidney (MDBK) cells in reinforced MEM medium (REM) containing 2 μ g/ml trypsin. MDBK cells were used for the plating of viruses and the study of virus
15 specific RNA synthesis.

6.1.2. PLASMIDS

In order to generate riboprobes, several plasmids were constructed. pSP64-NS DNA contains the entire NS
20 segment of A/WSN/33 virus inserted into the Sal I site of the pSP64 vector in the orientation by which mRNA sense NS RNA can be made using SP6 RNA polymerase.

The fragment derived from pSP64-NS by digestion with Hind III and Eco RI was inserted between the Hind III
25 and the Eco RI site of the IBI30 vector. The

resulting plasmid IBI30-NS can produce minus sense NS RNA using T7 RNA polymerase. In order to obtain

plasmid Δ T3NAV which produces minus sense NA specific RNA probe, the DNA in the pT3NAV plasmid (Enami et

30 al., 1990, Proc. Natl. Acad. Sci. USA 87: 3802-3805) was shortened by deleting the fragment between the Bam HI and the Eco RI sites. In addition, we created a

plasmid designated IBI30-NA by inserting the fragment between the Xba I and Eco RI sites of pT3NAV into the

35 IBI30 vector. This plasmid can generate positive sense NA specific RNA by T7 polymerase transcription.

6.1.3. VIRUS PURIFICATION AND RNA EXTRACTION

Influenza A/WSN/33 virus and NA/B-NS transfectant virus were grown in MDBK cells, and then purified through 30-60% sucrose gradient centrifugation as described previously (Enami et al., 1990, Proc. Natl. Acad. Sci. USA 87: 3802-3805). Virus purified from four 175 cm² flasks of MDBK cells was resuspended in 0.3 ml TMK buffer (10 Mm Tris, pH 7.5, 1.5 mM MgCl₂, 10 mM KCl) and disrupted by incubation with 9 µl 10% SDS and 7.5 µl proteinase K (10 mg/ml) at 56° C for 10 minutes, followed by addition of 35 µl SLN buffer (5% SDS, 1.4 M LiCl, 100 mM NaOAC, pH 7.0). Virion RNAs were extracted with phenol-chloroform and collected by ethanol precipitation. For isolating viral RNAs from infected cells, MDBK cells were infected with either influenza A/WSN/33 virus or NA/B-NS transfectant virus at an m.o.i.=1, and harvested at the indicated time points. Cells were washed twice with ice-cold PBS and lysed with 4 M guanidinium isothiocyanate (Sigma). The total RNA was then purified by equilibrium centrifugation in 5.7 M cesium chloride (Fisher) (Luo et al., 1991, J. Virol. 65: 2861-2867).

6.1.4. DETERMINATION OF THE RATIO OF INFECTIOUS AND PHYSICAL PARTICLES

In order to determine the total number of physical particles of influenza A/WSN/33 virus and NA/B-NS transfectant virus, the virus preparations were mixed with an equal volume of a suspension of carboxylate polystyrene beads (0.1 µ in diameter) at a concentration of 4.5 X 10⁹ particles per milliliter (Polyscience, Inc., Warrington, PA.), and then stained with phosphotungstic acid. The ratio of virus and polystyrene beads was determined by counting the two different particles under the electron microscope. For measuring the number of infectious particles in

the preparations, the virus stocks were serially diluted and plaqued in MDBK cells.

6.1.5. RNA ELECTROPHORESIS

5 RNAs extracted from influenza A/WSN/33 virus and NA/B-NS transfectant virus were electrophoresed on a 3% polyacrylamide gel containing 7.7 M urea at 150 volts for two hours. The RNA segments were visualized by silver staining as described previously (Enami
10 et al., 1990, Proc. Natl. Acad. Sci. USA 87: 3802-3805).

6.1.6. RIBONUCLEASE PROTECTION ASSAY

Ribonuclease protection assay (RPA) was used for
15 quantitation of virion RNA in viral particles as well as for the measurement of viral mRNAs and cRNAs in infected MDBK cells. The NS segment was chosen as an internal control. For measuring virion RNAs, positive sense NS and NA specific RNA probes were generated by
20 run-off transcription using phase SP6 or T7 RNA polymerase and plasmid PSP64-NS DNA linearized by Nco I and plasmid IBI30-NA digested with Fok I, respectively. To determine the amount of mRNAs and cRNAs, minus sense NS and NA specific RNA probes were
25 transcribed from Dde I digested IBI30-NS DNA and Pvu II cut Δ T3NA DNA, respectively, using phage T7 or T3 RNA polymerase respectively. The RNA probes were labelled with $\alpha^{32}\text{P}$ [UTP] (800 Ci/mM, Du Pont, NEN, Boston, MA). In general, 50 ng of virion RNA
30 extracted from purified virus was hybridized to 5×10^4 cpm each of positive sense NS and NA specific probes, or 5 μg of total RNA isolated from virus-infected cells was hybridized to 5×10^4 cpm each of minus sense NS and NA specific probes. After 12 hours
35 incubation at 45°C, the hybridization mixture was digested by RNase A/T₁, following the manufacturer's instruction (Ambion Inc., Austin, Texas), and the

resulting products were analyzed on a 6% acrylamide denaturing gel (Luo et al., 1990, J. Virol. 64: 4321-4328).

5 6.1.7. PRIMER EXTENSION

The genomic RNAs (vRNAs) of NA and NS segments of influenza A/WSN/33 virus and of NA/B-NS transfectant virus were quantitated by primer extension (Luo & Taylor, 1990, J. Virol. 64: 4321-4328). The primers for detecting NS and NA specific vRNA are 21 nt long and are complementary to minus sense vRNA. The NS primer, 5'-GGGAACAATTAGGTCAGAAGT-3', spans the region between nucleotides 695 to 714 of the NS cRNA. The NA primer, 5'-GTGGCAATAACTAATCGGTCA-3', covers the nucleotides 1151 to 1171 of the NA cRNA. Both NS and NA primers were 5'-end labelled by incubation with ³²P-ATP (3000 Ci/mM, Du Pont, NEN, Boston, MA.) and T4 DNA kinase (Biolabs, Beverly, MA.). 100 ng of RNA extracted from virus or 5 µg of total RNA isolated from infected MDBK cells was reverse transcribed by RNase H minus MLV reverse transcriptase (BRL, Gaithersburg, MD.) in the presence of 3 x 10⁵ cpm of each of 5'-end labelled NS and NA primers. After incubation at 37°C for 2 hours, the reaction was stopped by addition of EDTA to 10 mM, and followed by phenol-chloroform extraction and alkali treatment (Luo & Taylor, 1990, J. Virol. 64: 4321-4328). The products were analyzed on a 6% polyacrylamide gel containing 7 M urea. The amount of product was measured by directly counting the radioactivity of the gel piece corresponding to each band on the film.

6.1.8. NEURAMINIDASE ASSAY AND WESTERN ANALYSIS

35 For the assay of neuraminidase activity of influenza A/WSN/33 and NA/B-NS transfectant viruses, 2'-(4-methylumbelliferyl)- α -D-N-acetylneuraminic acid

(Sigma) was used as substrate. The reaction mixture consisted of 25 μ l 2 mM substrate, 25 μ l virus and 50 μ l 0.2 M phosphate buffer (pH 6.0) containing 2 mM CaCl_2 . After incubation at 37°C for 10 minutes, the reaction was stopped by addition of 2 ml 0.5 M glycine-NaOH buffer (pH 10.6), and then the neuraminidase activity was determined by measuring the fluorescence with excitation at 365 nm and emission at 450 nm, using methylumbeliferone as a standard. The protein concentration of the viruses was measured using the Bio-Rad protein assay kit. For the Western analysis of NA and HA proteins of WSN/33 and NA/B-NS viruses, viral proteins were electrophoresed on a 10% Laemmli gel (Laemmli, 1970, Nature 227: 680-685), and subsequently transferred to a nitrocellulose membrane (Schleicher & Schuell, Keene, NH). A monoclonal antibody directed against carbohydrates was used to detect the NA and HA glycoproteins of the viruses. The Western blot was developed with a rat antibody against mouse kappa chains which was labelled with ^{125}I iodine.

6.1.9. ANALYSIS OF PROTEIN SYNTHESIS IN INFECTED CELLS

MDBK cells (35 mm dish) were infected with either WSN/33 virus or NA/B-NS transfectant virus at an moi of approximately 3. This multiplicity was used because the NA/B-NS transfectant virus did not grow to higher titer. At indicated times, the proteins were labelled in cysteine free medium with [^{35}S]cysteine (1027 Ci/mmol, Du Pont, NEN Research Products) at 100 μ ci/ml medium for 30 minutes. The cells were then washed twice with ice-cold PBS buffer and lysed in 150 μ l lysis buffer containing 1% NP-40, 150 mM NaCl, 50 mM Tris-HCl pH 8.0, and 1 mM PMSF. About 1/20th of the sample was loaded onto a 10% Laemmli gel (Laemmli, 1970, Nature 227: 680-685).

10 **6.2.1. RATIO OF INFECTIOUS
TO PHYSICAL PARTICLES**

The genome of the transfectant NA/B-NS virus differs from wild type influenza A/WSN/33 virus only in the noncoding region of the NA gene. It is thus likely that the altered biological properties of the transfectant virus are the result of altered cis signals located in the noncoding region of the chimeric NA gene. Specifically, it was noted earlier that the transfectant virus grew to lower titers than wild type virus in MDBK cells, MDCK cells and in mice. In addition, the low multiplicity growth curves in tissue culture were significantly delayed relative to those of wild type virus (Muster et al., 1991, Proc. Natl. Acad. Sci. USA 88: 5177-5181). The transfectant virus was examined for a temperature sensitive phenotype, which could explain the altered growth characteristics. However, the pattern of the growth curve at 30°C, 33°C, 37°C and 38°C for NA/B-NS virus was not different from that of wild type virus at the corresponding temperatures. To answer the question of whether defective particles were present in the NA/B-NS virus preparation, the virus was characterized by counting the physical particles under the electron microscope and comparing this number with the plaque-forming units of the preparation. Interestingly, the NA/NS-B transfectant virus showed a similar number of physical particles as wild type virus, but

consistently lower PFU titers (Muster et al., 1991,
Proc. Natl. Acad. Sci. USA 88: 5177-5181) (Table II).

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TABLE II

The ratio of infectious particles to physical particles of influenza A/WSN/33 virus and NA/B-NS transfectant virus.

Viruses	No. of physical particles, (pp)	No. of infectious particles (ip)	Ratio pp/ip
WSN/33	1.8×10^9 /ml	1.2×10^8 /ml	15
NA/B-NS	1.2×10^9 /ml	1.0×10^7 /ml	120

Thus, the NA/B-NS virus grown in MDBK cells shows at least a 5 to 10-fold lower infectious particle to physical particle ratio than is seen with the WSN/33 wild type virus.

6.2.2. CHARACTERIZATION OF THE RNA OF THE ATTENUATED VIRUS

Since the NA/B-NS virus contains many defective particles, the viral RNA was examined for the presence of defective RNAs. Following extraction from purified virus, the genomic RNA was separated on a 3% polyacrylamide gel containing 7.7M urea. As shown in panel A of FIG. 2, the chimeric NA RNA of the NA/B-NS transfectant virus is almost invisible on the gel, whereas the other seven segments are present in approximately equimolar concentrations. When the amount of RNA was increased on the gel, the chimeric NA RNA can be shown to migrate at the same position as the control RNA in FIG. 2, lane 3. However, electrophoresis and silver staining did not permit the quantitation of the chimeric NA RNA packaged in virions. For this purpose, the ribonuclease protection assay (RPA) and primer extension experiments were performed. Positive sense NS-

specific and NA-specific probes were hybridized in the same reaction to purified virion RNA from either WSN/33 virus (FIG. 2, lane 2) or NA/B-NS transfectant virus (FIG. 2, lane 3) and then digested by RNase A/T₁.
5 The resulting products were analyzed on a 6% polyacrylamide gel containing 7M urea (Luo et al., 1991, J. Virol. 65: 2861-2867), and the amounts of vRNA were calculated by counting the radioactivity of the gel slices corresponding to the bands on the film.
10 As shown in panel B of FIG. 2, the probe protected by the chimeric NA RNA migrates faster than that of the wild type gene because the 5'-noncoding sequences are different in the two NA genes. When compared to the NA segment of WSN/33 virus, the amount of chimeric NA
15 RNA in the transfectant virus is about 6 times lower using the NS gene as an internal control. The primer extension experiment, as shown in panel C of FIG. 2, shows similar reduction of the chimeric NA RNA packaged in virions relative to the NS gene,
20 suggesting a specific lower representation of the chimeric NA gene in the transfectant virus preparation.

6.2.3. CHARACTERIZATION OF THE PROTEIN OF THE ATTENUATED VIRUS

25 To determine whether or not the NA/B-NS transfectant virus also contained less neuraminidase protein, neuraminidase assays and a Western analysis of the NA protein in virus particles were conducted.
30 For the enzymatic assay of the neuraminidase, the total concentration of viral proteins was first determined by protein assay, and then the same amount of purified virus was used. The NA/B-NS transfectant virus showed only a two-fold lower NA activity than
35 the WSN/33 wild type virus. A similar finding was obtained by Western analysis, which showed 1.9 fold less NA protein, but the same amount of HA protein in

virions of the NA/B-NS transfectant virus as compared to those of WSN/33 virus (FIG. 5, panel A).

6.2.4. VIRUS-SPECIFIC RNA SYNTHESIS IN INFECTED CELLS

5 Based on the vRNA analysis of the NA/B-NS transfectant virus, there is little doubt that less chimeric NA RNA is contained in the viral particles. The lower level of the chimeric NA RNA in the virions
10 could be caused either by a change in the packaging signal leading to less efficient packaging of the NA RNA or by a change in the synthesis of genomic NA RNA which could be the result of inefficient recognition of the influenza B virus specific promoter by the
15 influenza A viral polymerase. To pinpoint the exact mechanism, the synthesis of the chimeric NA gene in infected MDBK cells was examined. Considering that vRNA is mainly synthesized in the late phase of infection (Shapiro et al., 1987, J. Virol. 61: 764-
20 773), RNA was extracted from cells at 7, 8-1/2, and 10 hours post-infection. Five μ g of total RNA extracted from virus-infected cells was used for the primer extension analysis. The data in FIG. 4 show that vRNA synthesis of the chimeric NA gene was remarkably
25 decreased relative to that of control virus. When compared to the synthesis of the NA RNA of WSN/33 virus, the chimeric NA gene is reduced by a factor of 9, 8, and 8 at 7, 8-1/2, and 10 hours p.i., respectively. However, no reduction of vRNA synthesis
30 was observed with respect to the NS segment of the NA/B-NS transfectant virus. This result indicates that the reduction of the chimeric NA RNA in transfectant virus is the result of its lower synthesis in cells rather than due to a defect in the
35 packaging of the chimeric NA RNA.

 In order to determine the level of mRNA synthesis of the chimeric NA gene, MDBK cells were infected with

either WSN/33 virus or NA/B-NS transfected virus, and total RNA was then isolated from virus-infected cells at different times post-infection. Subsequently, the level of virus specific mRNAs was quantitated by RPA.

5 Again the NS segment was used as control (see FIG. 3). From the time course, it is apparent that the level of chimeric NA mRNA is markedly reduced relative to that of the wild type virus and that it only increases slightly with time. At 5 hours p.i., the level of

10 chimeric NA mRNA was five-fold less than that of WSN/33 virus (panel C), whereas the NS-specific mRNA synthesis of the NA/B-NS transfectant virus was similar to that of WSN/33 virus at the indicated times (panel B). It should be noted that the NS-specific

15 mRNA synthesis appears earlier and is more efficient than NA-specific mRNA synthesis in both WSN/33 and NA/B-NS transfectant virus infected cells (probes of similar activity were used in the experiment). This finding is in good agreement with previous reports

20 (Enami et al., 1985, Virology 142: 68-77), and suggests that the mRNA synthesis of different influenza virus RNA segments is differentially regulated. The conditions of the assay did not permit quantitation of the level of cRNA of the chimeric NA

25 gene because the cRNA synthesis was found to be only 3-5% of that of mRNA synthesis.

6.2.5. REDUCTION OF NA PROTEIN SYNTHESIS IN VIVO

30 The NA protein was found to be reduced by a factor of two in virions of the NA/B-NS transfectant virus, whereas the synthesis of chimeric NA mRNA was reduced by much more. The question then arose whether the NA protein encoded by the chimeric NA mRNA inside

35 cells parallels the amount of its mRNA, or whether there is a selective incorporation of the neuraminidase into the viral envelope. In order to

answer this question, the synthesis of NA protein in infected cells was measured. Viral proteins were labelled with ^{35}S [cysteine] at 1, 3, 5, and 7 hours post-infection. The cell lysates were then analyzed
5 on a 10% Laemmli gel (Laemmli, 1970, Nature 227: 680-685) and the proteins were quantitated by an AMBIS radioanalytic imaging system (Luo & Taylor, 1990, J. Virol. 64: 4321-4328). As shown in panel B of FIG. 5, synthesis of the NA protein of NA/B-NS transfectant
10 virus was two times lower than that of wild type virus at both 5 and 7 hrs p.i. From this experiment, it can be concluded that the assembly of the NA protein into virions parallels its synthesis in infected cells.

15 7. EXAMPLE: PANHANDLE BASE PAIRS
 INVOLVED IN ATTENUATION OF
 INFLUENZA VIRUS

 The experiments described below were designed to identify the nucleotide sequences responsible for attenuation and the effects of gene expression on
20 viral replication.

 7.1. MATERIALS AND METHODS

 The reverse genetics technique was used to engineer mutations into the panhandle structure of the
25 NA segment of influenza. Viruses and cells were prepared, purified and analyzed for attenuation as described in Section 6.1 and its subsections, supra.

30 7.2. RESULTS

 7.2.1. ATTENUATION SEQUENCE IN THE SECOND
 STEM STRUCTURE OF THE VIRAL PROMOTER

 A series of chimeric mutants construct d and analyzed for attenuation are shown in Table III below.
35 The results indicate that UCCU/AGGA of the NA/DeF/AbC influenza mutant are the critical base pairs involved in attenuation.

7.2.2. REDUCTION IN PROTEIN AND
ENZYME ACTIVITY

An additional attenuated mutant, designated NAM-3
has the following structure:

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      AG.A      A      UUUGAACAAACAUU
AGU      AAC.. AGGAGUUU
UCG      UUG    UCCUCAAA
      ...U      CG      CUUAC
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10 NAM 3, like NA/B-NS, demonstrates attenuation in that
defective particles are produced during each round of
replication. However, NAM 3 also demonstrated a ten-
fold decrease in neuraminidase expression and enzyme
activity (Table IV). This decrease in expression of
the enzyme did not affect viral replication.

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TABLE IV
NA EXPRESSION AND ACTIVITY
IN INFLUENZA VIRUS MUTANT

	<u>Strain</u>	<u>Protein¹</u>	<u>Enzyme Activity²</u>		
			<u>10 min</u>	<u>20 min</u>	<u>40 min</u>
10	WSN-wt	1.00	3.6	5.48	5.17
	NAM 3	0.14	0.19	0.26	0.67

- 15 ² Relative intensities of NA bands displayed on SDS-PAGE of infected cells. See Section 6.1.9 for Methods.
- 20 ² Virus was purified over sucrose containing Ca⁺⁺ as described in Section 6.1.3. Enzyme activity was assayed described in Section 6.1.8, and is expressed as percent substrate conversion by 1 ng virus/minute.

25 8. EXAMPLE: EXPRESSION OF FOREIGN EPITOPES IN THE ANTIGENIC SITES B OR E OF HA OF INFLUENZA RESULTS IN ATTENUATION

The experiments described below indicate that alterations to the B or E region of HA may be engineered to construct attenuated chimeric influenza viruses.

8.1. MATERIALS AND METHODS

The reverse genetics techniques described in Section 6.1.1. supra, were utilized to (a) introduce the malarial pitope (ME 1) of Plasmodium yoelii, (NEDSYVPSAEQI) into antigenic site E of the HA of

influenza (see FIG. 6A); or (b) to introduce the major antigenic determinant of poliovirus type 1, i.e. the BC loop of the VP1 of poliovirus type 1 (PASTTNKDKL), into antigenic site B of HA of influenza (see FIG.

- 5 6B). The LD₅₀ of chimeric and wild type influenza was determined in mice by the Karber method (see Muster et al., 1991, Proc. Natl. Acad. Sci. USA 88: 5177-5181).

10

8.2. RESULTS

The chimeric influenza/malaria virus had a 500-to 1000- fold lower LD₅₀ than that of wild type virus when assayed in mice. Likewise the chimeric influenza/polio virus demonstrated a lower LD₅₀.

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9. EXAMPLE: DELETIONS AND INSERTIONS OF THE STALK OF THE INFLUENZA VIRUS NEURAMINIDASE: GENERATION OF A HOST RANGE MUTANT

- Applying a reverse genetic system, the stalk of
20 the influenza A/WSN/33 virus neuraminidase (NA) gene was altered by making deletions, insertions and mutations in this region of the gene. The data presented in this example show that the length of the NA stalk can be variable. Interestingly, a deletion
25 of 28 amino acids resulted in a host range mutant virus with a markedly reduced growth rate in MDCK cells as compared to that in MDBK cells. Also, an insertion of 41 extra amino acids into the stalk did not significantly interfere with viral growth in
30 either MDCK or MDBK cells, suggesting that the stalk region can tolerate the introduction of long foreign epitopes.

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9.1. MATERIALS AND METHODS

9.1.1. CELLS AND VIRUS

Madin-Darby bovine kidney (MDBK) cells were used
5 for RNP transfection. Mardin-Darby canine kidney
(MDCK) and MDBK cells were used for preparation of
viruses as well as for determination of viral growth
characteristics. MDBK cells were grown in reinforced
minimal essential medium (REM) (Whittaker,
10 Walkersville, MD) supplemented with 10% FCS (GIBCO,
Gaithersburg, MD), and MDCK cells were grown in
minimal essential medium (MEM) (Whittaker) containing
10% FCS (GIBCO). MDBK and MDCK cells were maintained
in REM and MEM containing 0.42% bovine albumin (BA),
15 respectively. Influenza WSN-HK (H1N2) virus, a
reassortant virus, was used for the RNP transfection
experiment (Enami, et al., 1990, Proc. Natl. Acad.
Sci. USA 87:3802-3805). This virus has the NA gene of
influenza A/Hong Kong/8/68 virus and other seven RNA
20 segments from A/WSN/33 virus, and it does not grow in
MDBK cells in the absence of trypsin. WSN-HK virus
was propagated in 11 day old embryonated hens' eggs
and titrated in MDCK cells.

25 9.1.2. CONSTRUCTION OF NA MUTANTS

Clone pT3NAv which contains the cDNA of the
influenza A/WSN/33 virus NA gene was described
previously (Enami et al. 1990, Proc. Natl. Acad. Sci.
USA 87:3802-3805). No unique restriction enzyme site
30 was found in the region encoding the stalk of the NA
protein. In order to facilitate the manipulation of
the stalk of the NA, plasmid pT3NAv had to be
modified. One of the choices was destroy the Sty
I/Dsa I site at nucleotide 875 so that the Sty I site
35 at nucleotide 169 and the Dsa I site at nucleotide 253
became unique. For achieving this, th pT3NAv DNA was
cut by Nco I at nucleotide 875 and trimmed with

mungbean nuclease using standard methods (Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The DNA was then digested by Pst I at nucleotide 926. The fragment between nucleotides 875 and 926 was replaced by a polymerase chain reaction (PCR) fragment in which nucleotide 877 was changed by a silent mutation. The PCR fragment was made (Erlich, 1989, PCR Technology: Principles and Applications for DNA Amplification, Stockton Press) using pT3NAv as template and oligonucleotides NA01 and NA02 as primers (Table V). After digestion with Pst I, the PCR fragment was ligated into the pT3NAv DNA which was digested by both Nco I and Pst I. The modified pT3NAv was called pT3NAmod. Using the pT3NAmod clone, a series of NA mutants with deletions, insertions and mutations in the stalk region of the NA protein were generated. The oligonucleotides used for making these constructs are shown in Table V:

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TABLE V
CONSTRUCTION OF NA MUTANTS

5			Method of Construction*
	<u>Mutants</u>	<u>Oligonucleotides</u>	
	T ₃ NAmod	NA01 5'-CCTGGGTGTCCTTC-3' NA02 5'-CCCCACTGCAGATG-3'	PCR
10	Del 16	NA03 5'-CAAGGCAGCACCGGCAA <u>CTCGAGTCTTTGTCCCATC</u> -3' NA04 5'-CACGGATGGGACAAAGA <u>CTCGAGTTGCCGGTGCTGC</u> -3'	Annealing
	Del 18m	NA05 5'-GCGCGCTCGAGAGGCTGCC TTGG-3' M 13 5'-GTAAAACGACGGCCAGT-3'	PCR
15	Del 23N	NA06 5'-GCGCGCTCGAGTTGCCGGTA GTATGGTTTIG-3' M 13 See Above	PCR
	Del 23C	NA07 5'-GCGCGCCACGGCAAAGAGATGA ATTGTTGCATATTCC-3' M13 See Above	PCR
20	Del 28N	NA08 5'-GCGCGCTCGAGTTGCCGGTTC CGGTTTGAAT-3' M13 See Above	PCR
	N72Q/ C76S	NA09 5'-GCGCGCCACGGATGGGCGAAAGA GATGATTGGCCGGTTAATATC-3' M13 See Above	PCR
25	Ins 12	NA10 5'-CTTGGATGGGACAAAGACTCGAG TTGCCGGTGCTGC-3' NA03 See Above	Annealing
	Ins 41	NA11 5'-GCGCGCCGTGGGACCGGAA ATC-3' NA12 5'-AGCCCACCCACGG-3'	PCR
30			

* For all PCR reactions, pT3NAv was used as template.

The underlined nucleotides indicate the position of a newly created Ava 1 site.

Del 16 was created by replacing the fragment between the Sty I and Dsa I sites in pT3NAmoD with the annealed oligonucleotides NA03 and NA04. Through silent mutations, a unique Ava I site was created in plasmid Del 16 (underlined nucleotides in Table V). Mutant Del 18m, Del 23N and Del 28N was made by PCR using pT3NAV as template and M13/Puc forward sequencing primer (5'-GTAAAACGACGGCCAGT-3') and NA05, NA06 and NA08 as primer, respectively. The PCR products were digested by EcoR I and Ava I and inserted into plasmid Del 16 DNA which was digested by the same enzymes. Mutant Del 23C and N72Q/C76S were also made by PCR in the same way except for using NA07 and NA09 as primer, respectively. The PCR products were digested with Dsa I and Eco RI, and inserted into pT3NAmoD digested with the same enzymes. Ins. 12 and Ins 24 were obtained by inserting the annealed oligonucleotides NA03 and NA10 into the Sty I site of pT3NAmoD. Ins 24 contains a duplicate of the insertion present in Ins 12. Ins 41 was made by PCR using pT3NAV as template and oligonucleotides NA11 and NA12 as primers. The PCR fragment was digested by Dsa I and inserted into the Dsa I site of pT3NAmoD. In order to make Del 28 C, plasmid pT3NAmoD was cut by Dsa I, and filled-in with reverse transcriptase (BRL, Bethesda, Maryland). The DNA was then digested by Sty I, trimmed with mungbean nuclease and blunt-end ligated.

9.1.3. RNP TRANSFECTION

The RNP transfection experiments were carried out by using the standard protocol as reported before (Enami and Palese, 1991, J. Virol. 65:2711-2713). Briefly, the plasmid DNAs were digested by restriction enzyme Ksp6321 or Ear I. 1 µg linearized DNA was incubated in 10 µl viral nucleoprotein and polymerase proteins (approximately 1 µg) isolated from influenza

A/PR/8/34 virus and 100 U T3 RNA polymerase (Stratagene, La Jolla, CA) in a 50 μ l volume under transcription conditions. The in vitro reconstituted RNP complex was then transfected into MDBK cells which
5 were infected with WSN-HK reassortant virus at an mode of infectivity (m.o.i.) =1. At 20 hours post infection, the supernatant was collected and used for plaque assay in MDBK cells in order to select the transfectant virus.

10

9.1.4. VIRUS PREPARATION AND RNA EXTRACTION

Transfectant viruses were isolated and amplified from individual plaques in MDBK cells. Then viruses
15 were propagated in 175 cm² large flasks of MDCK cells, and purified through 30-60% sucrose gradients. Virion RNA was extracted from purified viruses as described previously (Luo et al., 1992, J. Virol. 66:4679-4685).

20

9.1.5. ELECTROPHORESIS AND SILVER STAINING OF vRNA SEGMENTS

The vRNA extracted from viruses was analyzed on a 2.8% acrylamide gel containing 7.7 M urea. The vRNA segments were then visualized by silver staining as reported before (Enami et al., 1990, Proc. Natl. Acad.
25 Sci. USA 87:3802-3805).

9.1.6. REVERSE TRANSCRIPTION AND PCR

The NA-specific RNA of the viruses containing wild type NA or Del 18m, Del 23N and Del 28N mutant
30 NAs were transcribed by reverse transcriptase (BRL, Bethesda, MD) using oligonucleotide 5'-GTCAATCTGTATGGTAGTCGG-3' as primer, which covers nucleotide 52 to nucleotide 72. The reverse transcripts were amplified by PCR using the above
35 oligonucleotide and oligonucleotide NA12 (Table V) as primers (Luo et al., 1991, J. Virol. 65:2861-2867).

5 9.1.7. GROWTH CURVE

MDBK and MDCK cells were infected with wild type virus and each of the transfectant viruses at an m.o.i.=0.001, and maintained in REM and MEM media containing 0.5 μ g/ml trypsin. Supernatants were collected at 12, 24, 36 and 48 hour postinfection. The number of plaque forming units (PFU) of each supernatant was determined by plaque assay in MDBK cells.

15 **9.2. RESULTS**

The influenza virus neuraminidase (NA) protein functions during the infectious cycle as an enzyme to remove terminal sialic acids. Its action may prevent self-aggregation of virus particles, and promote virus release during budding from host cells (Palese et al., 1974, *Virology* 61:397-410). NA is an integral membrane glycoprotein anchored in the viral membrane as a homotetramer. Each tetrameric NA appears as a mushroom-shaped spike (FIG. 7) on the surface of the virion when viewed in the electron microscope (Laver and Valentine, 1969, *Virology* 38:105-119; Wrigley et al., 1973, *Virology* 51:525-529). Structurally, the monomer of the NA consists of four different domains (FIG. 7): a cytoplasmic and a transmembrane domain, the thin stalk, and the globular head (Blok and Air, 1982, *Biochemistry* 21:4001-4007; Colman, 1989, in "The Influenza Viruses", R.M. Krug, ed., pp. 175-218, Plenum Press, NY). Although much is known about the structure and role of the head region, the structure-function relationship of the stalk region is less well understood. Presented below is a study of the stalk region of the NA in which the length and structure of

the stalk is varied by deletions, insertions and mutations.

9.2.1. RESCUE OF DELETION MUTANTS OF
NA INTO INFECTIOUS VIRUS

5 Based on sequence comparisons of different
influenza A virus NA genes, it has been suggested that
the stalk region of the NA varies between 25 and 57
amino acids (Blok and Air, 1982, Biochem. 21:4001-
10 4007; Blok and Air, 1982, Virol. 118:229-234; Els et
al., 1985, Virol. 142:241-247; Colman, 1989, in "The
Influenza Viruses", R.M. Krug, ed., pp. 175-218,
Plenum Press, NY). The stalk region of the influenza
A/WSN/33 virus NA, which was used in this study, is
15 approximately 41 amino acids long (Blok and Air, 1982,
Biochem. 21:4001-4007; Blok and Air, 1982, Virol.
118:229-234; Hiti and Hagar, 1982, J. Virol. 41:730-
734; Colman, 1989, in "The Influenza Viruses", R.M.
Krug, ed., pp. 175-218, Plenum Press, NY). It was
20 first asked whether NA mutants with large deletions
could be rescued into infectious virus particles. The
first mutant gene, Del 16, that was constructed lacked
48 nucleotides (amino acid position 53-69) (FIG. 8),
and following RNP transfection infectious virus was
25 isolated. Purified RNA was separated on a 2.8%
acrylamide gel containing 7.7 M urea and the NA
segment with the 48 nucleotide deletion (Del 16) was
shown to migrate faster than the NA RNA of the wild
type virus (FIG. 9: compare lane 1 and lane 2). This
30 suggested that influenza A/WSN/33 virus can tolerate a
neuraminidase with a stalk of only about 25 amino
acids. A gene encoding an NA with a 28 amino acid
deletion (Del 28C, FIG. 8) was then constructed.
After RNP transfection, however, no infectious virus
35 was rescued. This result could be either due to the
truncation of the stalk region or due to the deletion
of a potential glycosylation site at position 74

and/or of a cysteine at position 76. Since the potential glycosylation site and the cysteine residue are highly conserved among different NAs (Blok and Air, 1982, Biochem. 21:4001-4007), the possibility was first explored that important structural elements were destroyed by this deletion. For this purpose, three other NA mutants were constructed: N72Q/C76S, Del 23C, and Del 18m (FIG. 8). In the N72Q/C76S mutant, the asparagine (N) at position 72 and the cysteine (C) at position 76 were mutated into glutamine (Q) and serine (S), respectively. Although this gene has the same length of the stalk as the wild type gene, no infectious virus could be rescued. To dissect the contribution of the glycosylation site and of the cysteine residue, mutant Del 18m was constructed by changing the asparagine at position 72 to leucine and deleting amino acids 53 to 71. Interestingly, infectious progeny virus was obtained following RNP transfection of the Del 18m NA RNA. This finding suggests that the cysteine at position 76, rather than the potential glycosylation site at position 72 is essential for the formation of infectious virus. However, it was not clear whether or not deletions beyond the cysteine can be tolerated. Thus mutant Del 23C was designed in which the potential glycosylation site and the cysteine were reintroduced into the NA but two amino acids C-terminal to the cysteine were deleted. No virus containing the Del 23C mutant gene was obtained. It thus appears that the sequence following the stalk region does not tolerate deletions, suggesting that this region is part of the NA "head". However, the possibility could not be ruled out that the Del 23C mutant virus was non-infectious due to the further shortening of the NA stalk by 5 amino acids. Two more constructs were therefore created: Del 23N and Del 28N. The Del 23N mutant has a 23 amino acid deletion between amino acid

47 and 69, and the Del 28N mutant has a 28 amino acid deletion starting at amino acid 42 and extending to amino acid 69. Both Del 23N and Del 28N resulted in infectious influenza viruses. This suggests that an NA stalk of approximately 12 amino acids suffices to generate infectious virus. The deletion analysis was not extended further because the virus containing the Del 28N mutant NA does not grow as well as wild type virus (see below), and has a deletion that leaves only a few amino acids near the viral membrane at the N-terminal and the cysteine at the C-terminal side. In order to verify that the NA RNAs of the mutant viruses had truncated stalk regions, the NA specific RNAs were reverse transcribed and analyzed by PCR using a labelled primer. The sizes of the PCR products of wild type, Del 18m, Del 23N and Del 28N were as expected (FIG. 10, lanes 2-5).

9.2.2. RESCUE OF INSERTION MUTANTS OF NA INTO INFECTIOUS VIRUS

The deletion analysis revealed that the length of the NA stalk is flexible. Virus is still viable even when it contains an NA whose stalk region is almost completely deleted. The question, however, remained as to whether or not the stalk of the NA molecule can tolerate the insertion of extra amino acids. To answer this 12 and 24 amino acids were inserted into the stalk region of the NA between amino acids 50 and 51, as shown in FIG. 8 (Ins. 12 and Ins. 24, respectively). After RNP transfection, both Ins 12 and Ins 24 mutant NA RNAs were rescued into infectious transfectant viruses. The fact that these two NA mutants were viable, led the insertion of additional amino acids. To that end, mutant Ins 41 NA was generated by inserting 41 amino acids between position 39 and 40. The Ins 41 mutant contains a duplication in the NA stalk. Again, infectious virus was rescued,

indicating that the NA stalk tolerates a 41 amino acid insertion. The purified RNAs of Ins 12, Ins 24 and Ins 41 mutant viruses were analyzed on a polyacrylamide gel and the rescued NA RNAs were found to migrate in the expected positions (FIG. 9, lanes 3, 4, and 5).

9.2.3. GROWTH CHARACTERISTICS OF THE NA TRANSFECTANT VIRUSES

10 In order to determine whether deletions and insertions in the stalk region of the NA molecule have effects on virus growth, the transfectant viruses were characterized in MDBK and MDCK cells. The results are shown in FIG. 11. Since all mutant viruses were
15 rescued by isolating progeny viruses in MDBK cells to allow selection against the helper virus, it is not surprising that all mutants grow in this cell type (FIG. 11A). It appears that mutant Del 28N and mutant Ins 24 grow slightly slower and to lower titers than
20 do either the remaining mutants or the wild type virus. It should also be noted that the MDBK cell line currently in use yields lower overall titers than other MDBK cell lines. The yields in MDCK cells (FIG. 11B) are higher by approximately one log, except
25 those of mutant Del 18m and mutant Del 28N, which grow to 10^2 and 10^4 time lower titers, respectively, than does wild type virus. Mutant Del 28N is thus a host range mutant which grows about 1,000 times less efficiently in MDCK cells as compared to MDBK cells.

30 The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the invention, and any constructs or viruses which
35 are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described

herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

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WHAT IS CLAIMED IS:

1. An attenuated genetically engineered segmented RNA virus containing at least one modified
5 non-coding region that down-regulates synthesis of at least one viral gene segment, so that at least some defective particles are produced during each round of viral replication in a host.
- 10 2. The attenuated virus of Claim 1 which is a single stranded negative-sense RNA virus.
3. The attenuated virus of Claim 2 which belongs to the Orthomyxoviridae family.
15
4. The attenuated virus of Claim 2 which belongs to the Bunyaviridae family.
5. The attenuated virus of Claim 2 which
20 belongs to the Arenaviridae family.
6. The attenuated virus of Claim 3 which is an influenza virus.
- 25 7. The attenuated virus of Claim 1 which is a double-stranded RNA virus.
8. The attenuated virus of Claim 7 which is a reovirus.
30
9. The attenuated virus of Claim 7 which is a rotavirus.
10. The attenuated virus of Claim 7 which is a
35 orbivirus.

11. The attenuated virus of Claim 1 in which the modified non-coding region down-regulates synthesis of a viral capsid gene.

5 12. The attenuated virus of Claim 1 in which the modified non-coding region down-regulates synthesis of a viral envelope gene.

10 13. The attenuated virus of Claim 1 in which the modified non-coding region down-regulates synthesis of a viral protease gene.

15 14. The attenuated virus of Claim 1 in which the modified non-coding region down-regulates synthesis of a viral polymerase gene.

15 15. An attenuated genetically engineered negative-sense RNA virus containing at least one modified non-coding region that down-regulates transcription of at least one viral gene, so that the progeny virions produced during replication result in a subclinical level of infection in a host.

25 16. The attenuated virus of Claim 15 which is a segmented negative-sense RNA virus.

17. The attenuated virus of Claim 16 which belongs to the Orthomyxoviridae family.

30 18. The attenuated virus of Claim 16 which belongs to the Bunyaviridae family.

19. The attenuated virus of Claim 16 which belongs to the Arenaviridae family.

35

20. The attenuated virus of Claim 17 which is an influenza virus.

21. The attenuated virus of Claim 15 which is a non-segmented negative-sense RNA virus.

22. The attenuated virus of Claim 21 which
5 belongs to the Paramyxoviridae family.

23. The attenuated virus of Claim 21 which belongs to the Rhabdoviridae family.

10 24. The attenuated virus of Claim 15 in which the modified non-coding region down-regulates transcription of a viral capsid gene.

25. The attenuated virus of Claim 15 in which
15 the modified non-coding region down-regulates transcription of a viral envelope gene.

26. The attenuated virus of Claim 15 in which the modified non-coding region down-regulates
20 transcription of a viral protease gene.

27. The attenuated virus of Claim 15 in which the modified non-coding region down-regulates transcription of a viral polymerase gene.
25

28. An attenuated genetically engineered double-stranded RNA virus containing at least one modified non-coding region that down-regulates transcription of at least one viral gene, so that the progeny virions
30 produced during replication result in a subclinical level of infection in a host.

29. The attenuated virus of Claim 28 which is a reovirus.
35

30. The attenuated virus of Claim 28 which is a rotaovirus.

31. The attenuated virus of Claim 28 which is a orbivirus.

32. The attenuated virus of Claim 28 in which
5 the modified non-coding region down-regulates
transcription of the viral capsid gene.

33. The attenuated virus of Claim 28 in which
the modified non-coding region down-regulates
10 transcription of the viral envelope gene.

34. The attenuated virus of Claim 28 in which
the modified non-coding region down-regulates
transcription of the viral protease gene.

15

35. The attenuated virus of Claim 28 in which
the modified non-coding region down-regulates
transcription of the viral polymerase gene.

20 36. An attenuated genetically engineered
negative-sense RNA virus containing at least one
modified viral gene sequence that encodes at least one
insertion, deletion or substitution of an amino acid
residue or epitope so that the progeny virions
25 produced during replication result in subclinical
levels of infection in a host.

37. The attenuated virus of Claim 36 which is a
segmented negative-sense RNA virus.

30

38. The attenuated virus of Claim 37 which is an
influenza virus.

35 39. The attenuated virus of Claim 36 which is a
non-segmented negative-sense RNA virus.

40. The attenuated virus of Claim 36 in which a viral structural gene is modified.

41. The attenuated virus of Claim 40 wherein the
5 viral structural gene is a neuraminidase gene.

42. The attenuated virus of Claim 41 wherein the attenuated virus is an influenza virus.

10 43. The attenuated virus of Claim 41 wherein a stalk domain coding region of the neuraminidase gene is modified.

44. The attenuated virus of Claim 43 wherein the
15 attenuated virus is an influenza virus.

45. The attenuated virus of Claim 36 in which a viral non-structural gene is modified.

20 46. The attenuated virus of Claim 36 in which the modified viral gene sequence encodes at least a portion of the viral gene and a foreign epitope so that a chimeric protein is expressed in the infected host.

25 47. The attenuated virus of Claim 38 in which the modified viral gene sequence encodes at least a portion of the viral gene and a foreign epitope so that a chimeric protein is expressed in the infected
30 host.

48. The attenuated virus of Claim 40 in which the modified viral gene sequence encodes at least a portion of the viral gene and a foreign epitope so
35 that a chimeric protein is expressed in the infected host.

49. The attenuated virus of Claim 41 in which the modified viral gene sequence encodes at least a portion of the viral gene and a foreign epitope so that a chimeric protein is expressed in the infected
5 host.

50. The attenuated virus of Claim 49 wherein the attenuated virus is an influenza virus.

10 51. An attenuated genetically engineered double-stranded RNA virus containing at least one modified viral gene sequence that encodes at least one insertion, deletion or substitution of an amino acid residue or epitope so that the progeny virions
15 produced during replication result in subclinical levels of infection in a host.

52. The attenuated virus of Claim 51 which belongs to the reoviridae family.

20

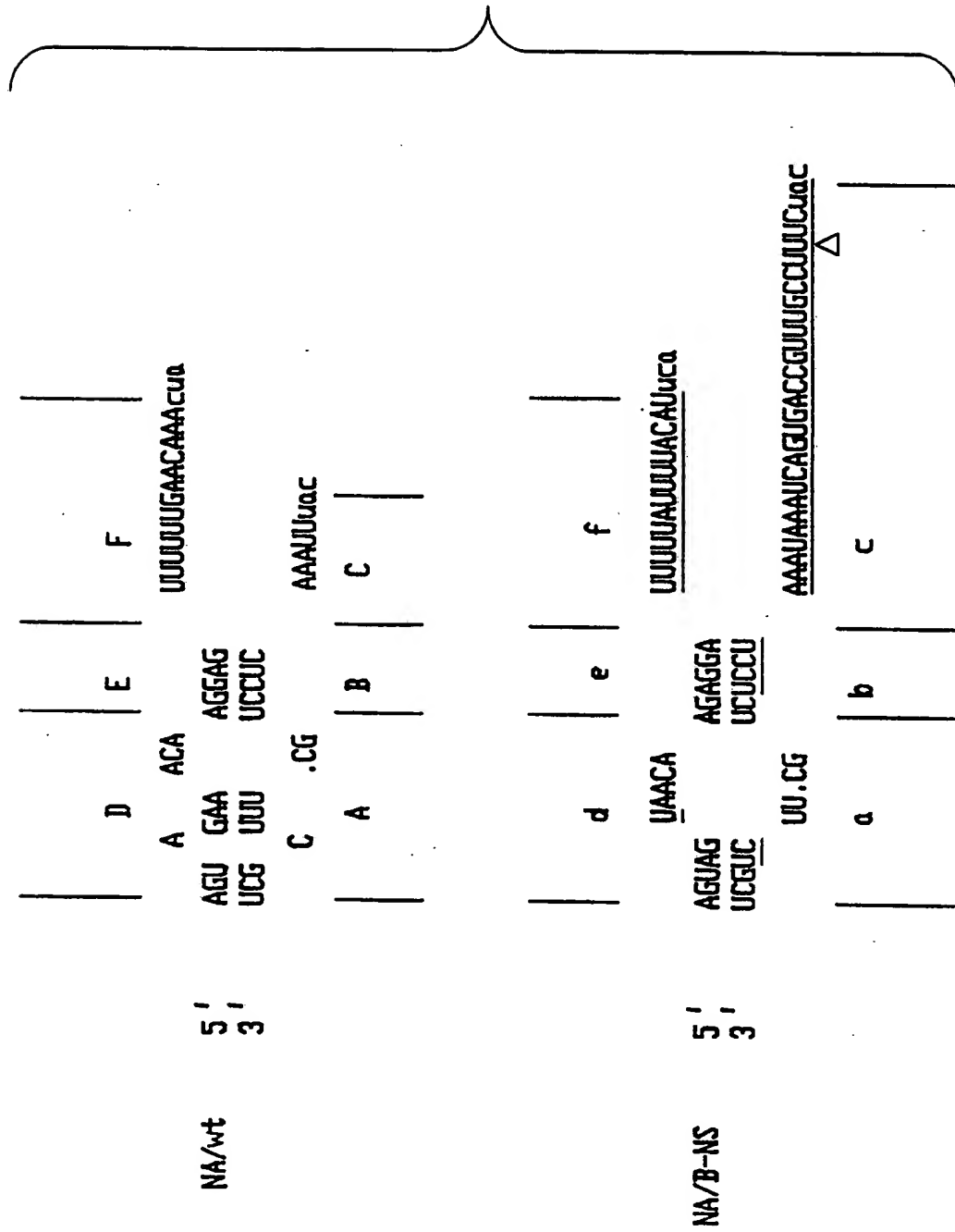
53. The attenuated virus of Claim 51 in which a viral structural gene is modified.

54. The attenuated virus of Claim 51 in which a
25 viral non-structural gene is modified.

55. The attenuated virus of Claim 51 in which the modified viral gene sequence encodes at least a portion of the viral gene and a foreign epitope so
30 that a chimeric protein is expressed in the infected host.

56. The attenuated virus of Claim 53 in which the modified viral gene sequence encodes at least a
35 portion of the viral gene and a foreign epitope so that a chimeric protein is expressed in the infected host.

FIG.1



2 / 14

WSN/33 NA/B-NS CONTROL

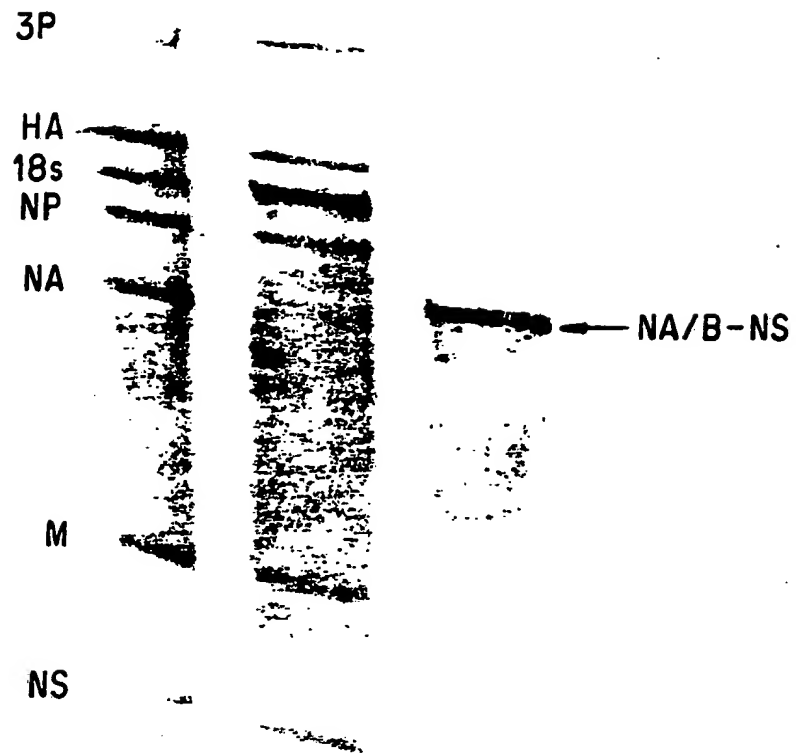


FIG. 2A

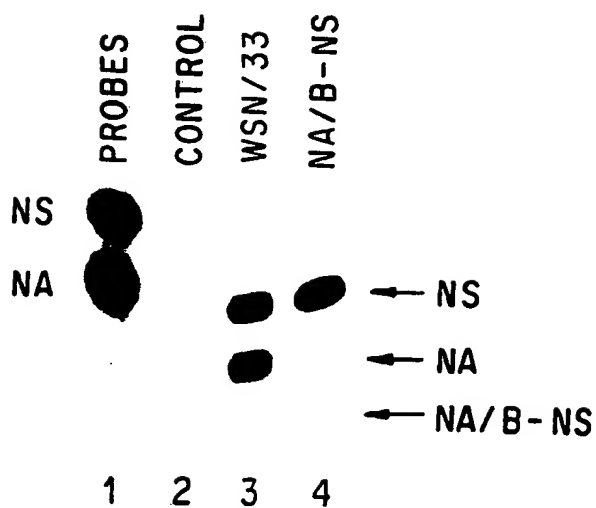


FIG. 2B

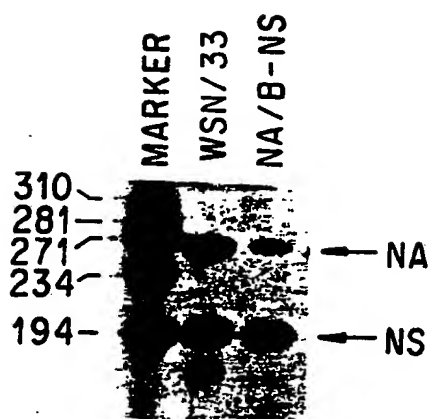


FIG. 2C

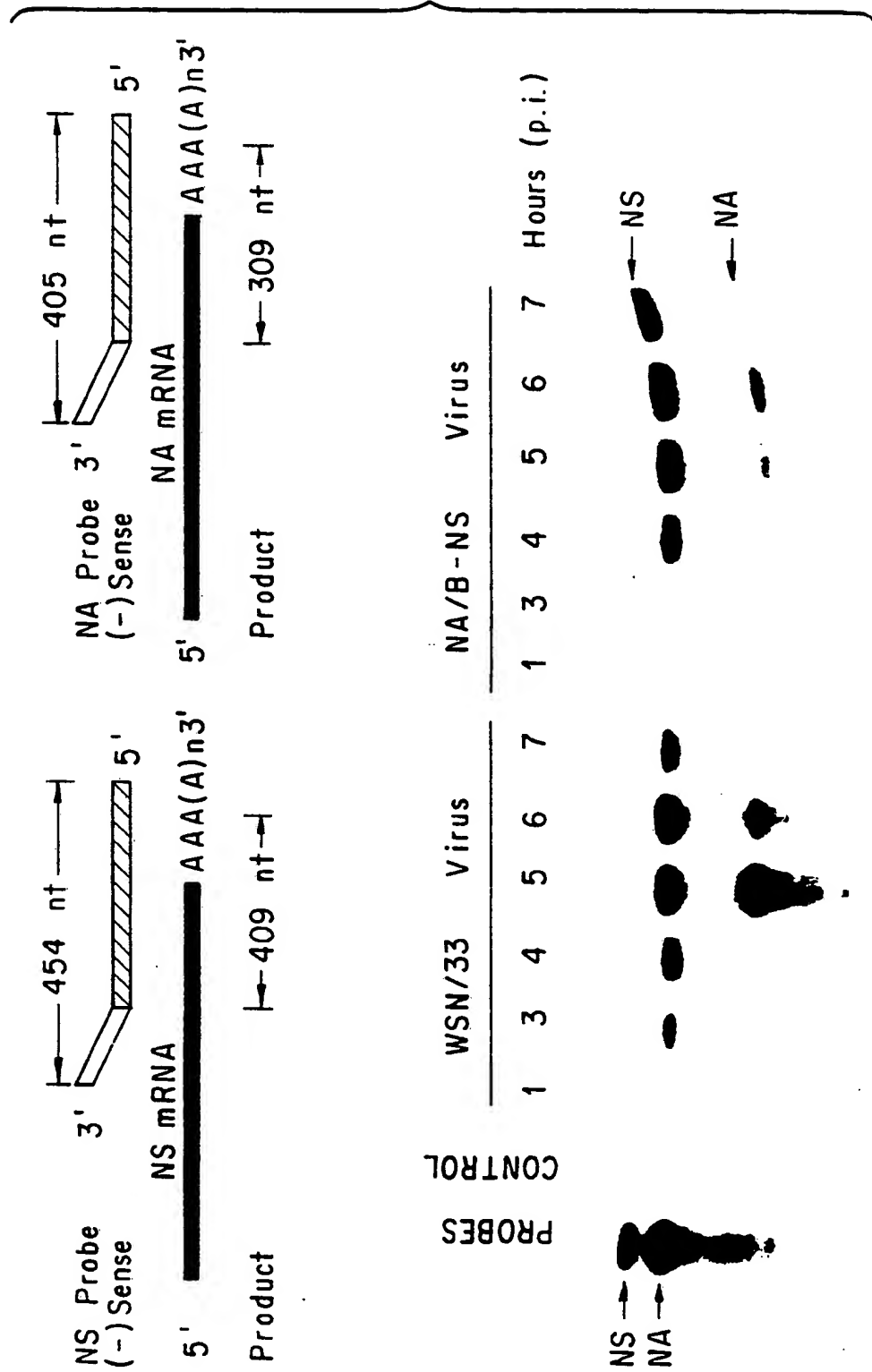


FIG. 3A

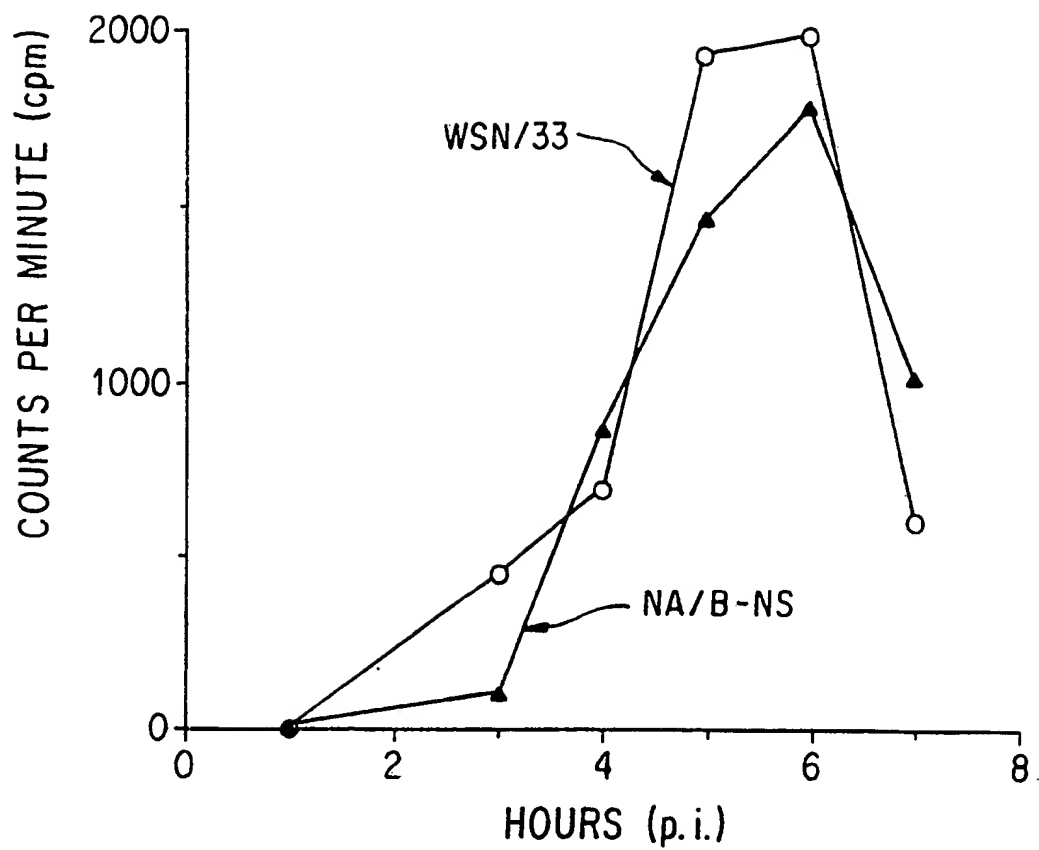


FIG. 3B

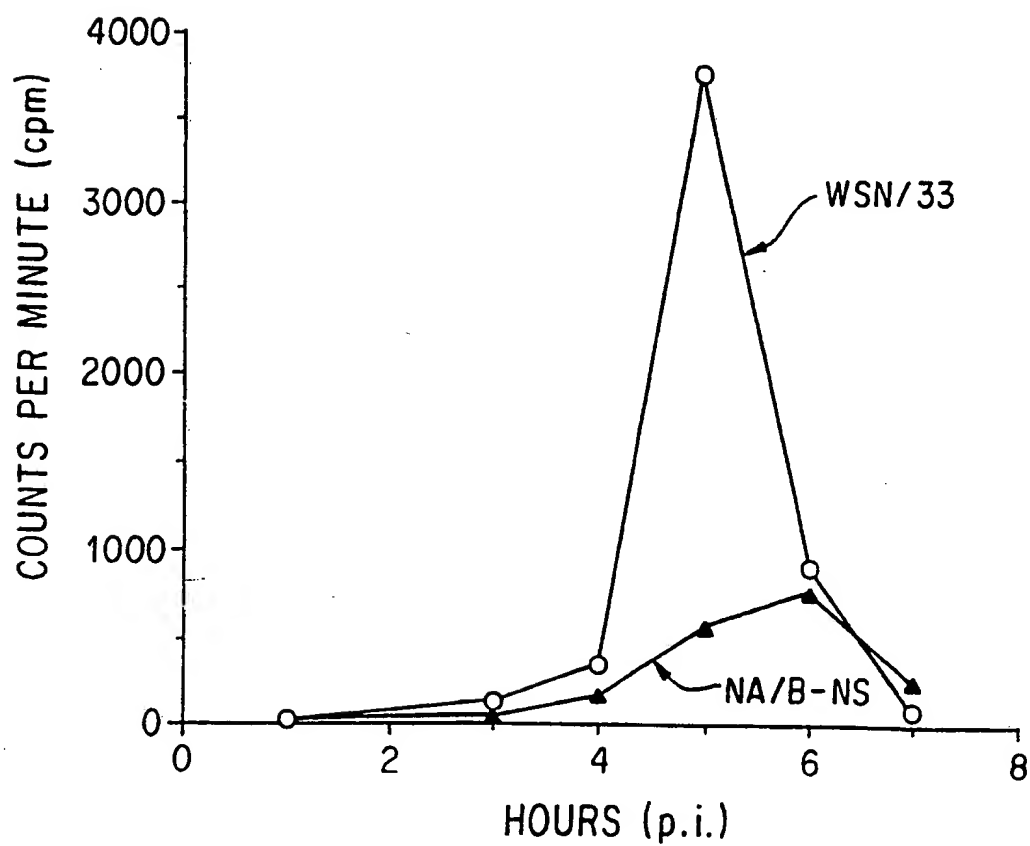


FIG. 3C

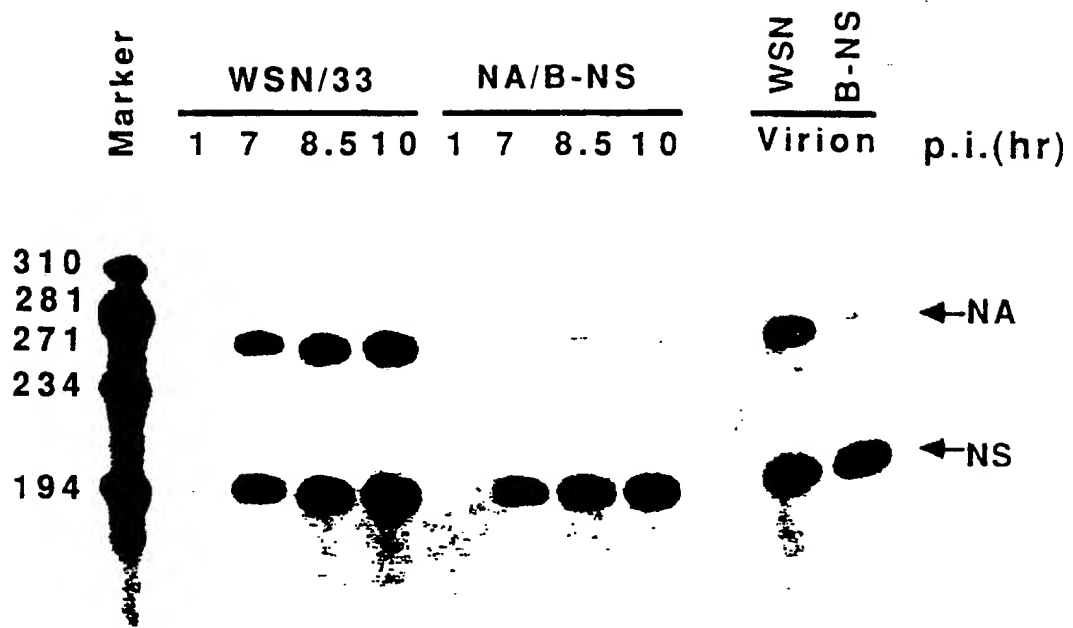


FIG. 4

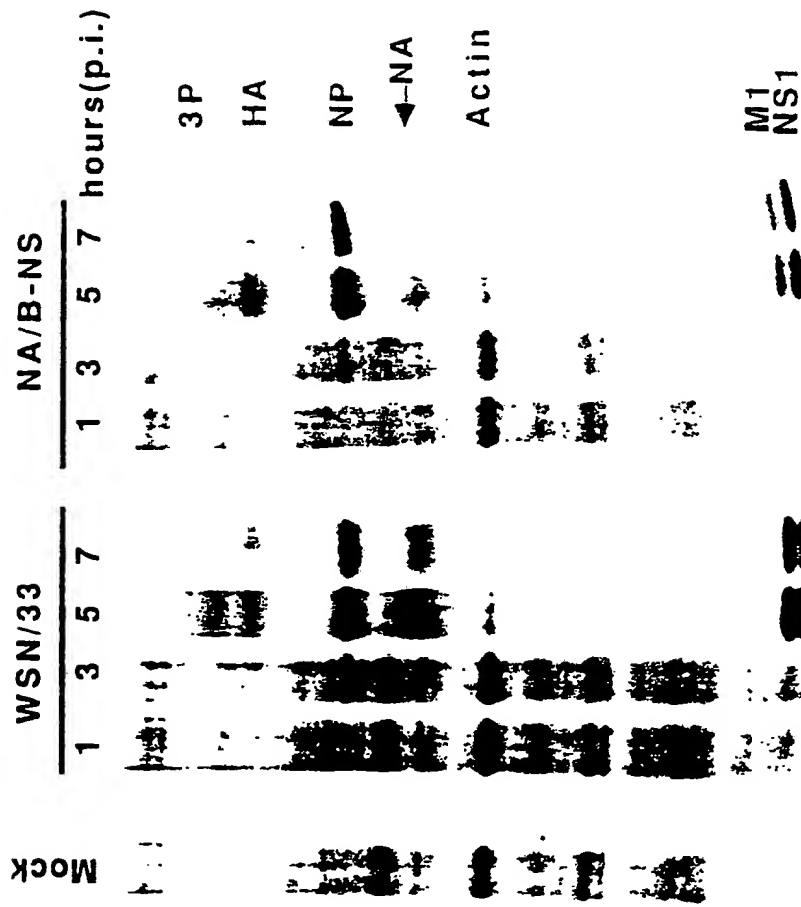


FIG. 5B

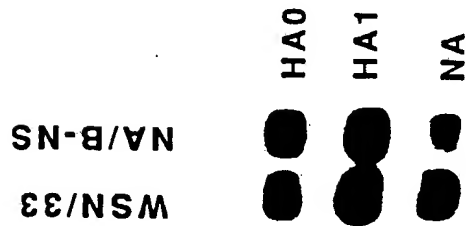
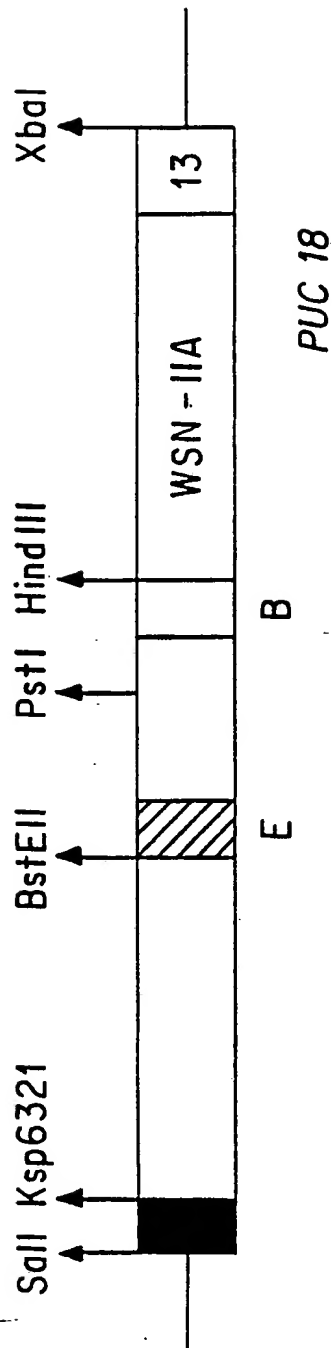


FIG. 5A



A. WSN site E: CD SLLPARS W SYI

MALARIA ME1: C NEDSYVPSAEQI W SYI

B. WSN site B: WLT KKGDSYP KLT

POLIO 1 (BC loop): WLT KKG PASTTNKDKL DSYP KLT

FIG. 6

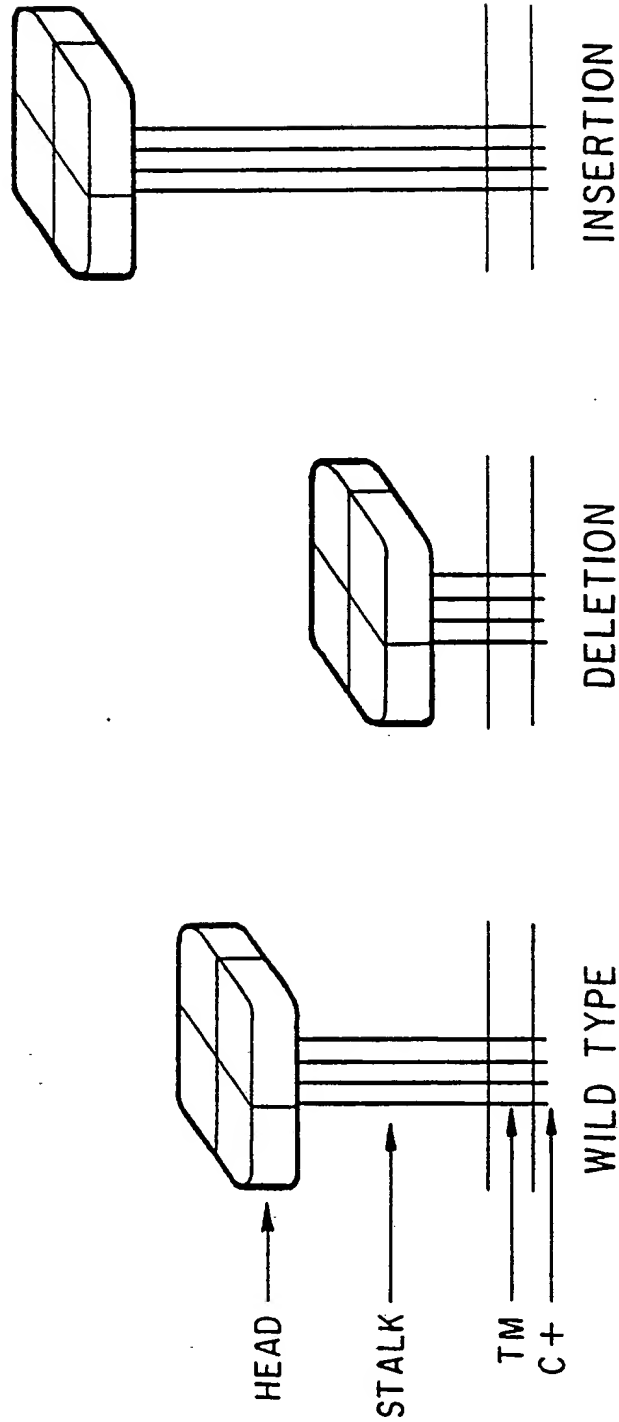
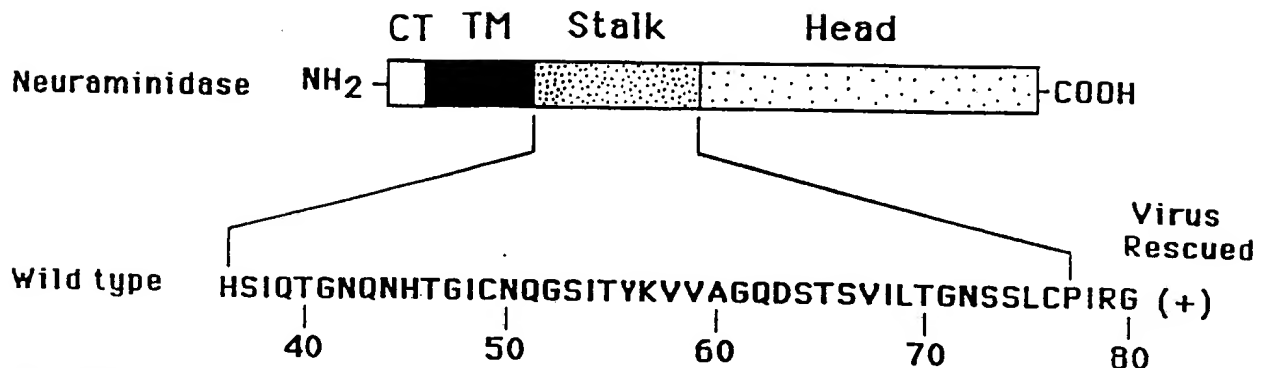


FIG. 7

Deletion

Del 16	HSIQTGNQNHTGICNQGS-----TGNSSLCPIRG (+)
Del 28C	HSIQTGNQNHTGICN-----RG (-)
Del 18m	HSIQTGNQNHTGICNQGS-----L SSLCPIRG (+)
Del 23C	HSIQTGNQNHTGICN-----NSSLC--RG (-)
Del 23N	HSIQTGNQNHT-----TGNSSLCPIRG (+)
Del 28N	HSIQTG-----TGNSSLCPIRG (+)

Insertion

Ins 12	CN QGSTGNSSLCPI QGSIT 50 51	(+)
Ins 24	CN QGSTGNSSLCPIQGSTGNSSLCPI QGSIT 50 51	(+)
Ins 41	Q TGNQNHTGICNQGSIYKVVAGQDSTSVILTGNS SLCP IRG T 39 40	(+)

Mutation

N72Q/C76S	HSIQTGNQNHTGICNQGSIYKVVAGQDSTSVILTGQSSLSPIRG (-)
	40 80

FIG. 8

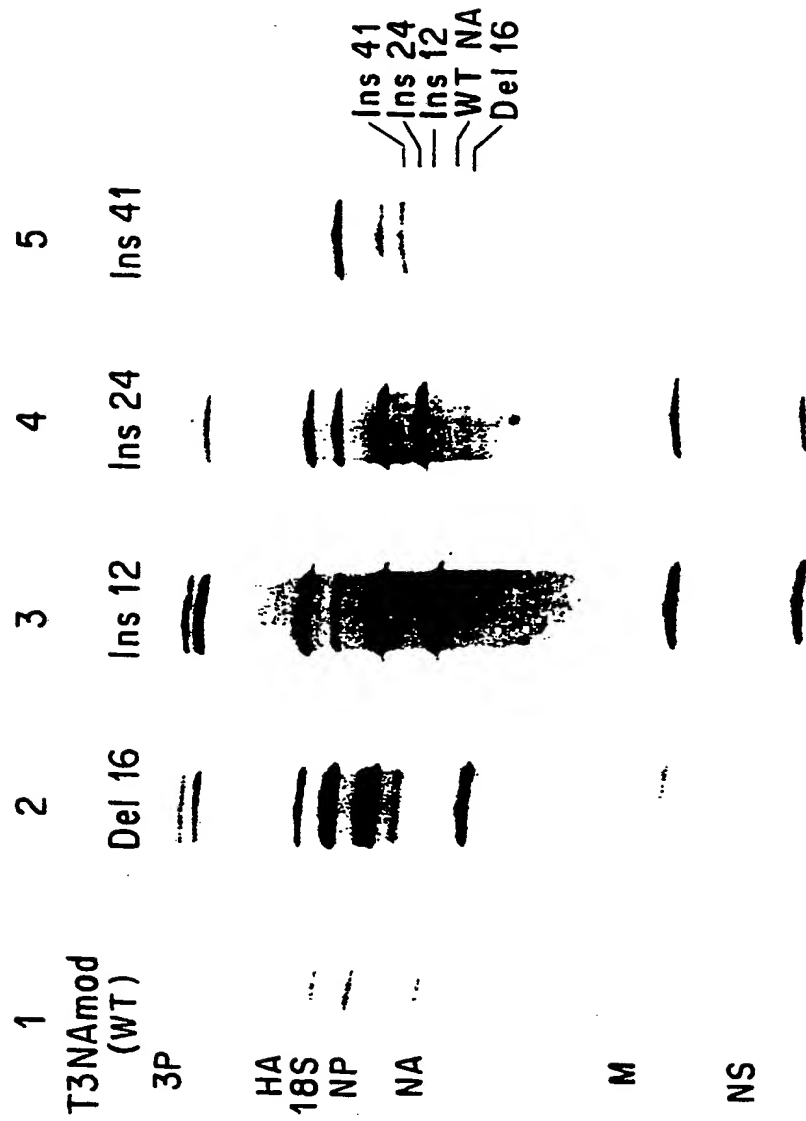


FIG. 9

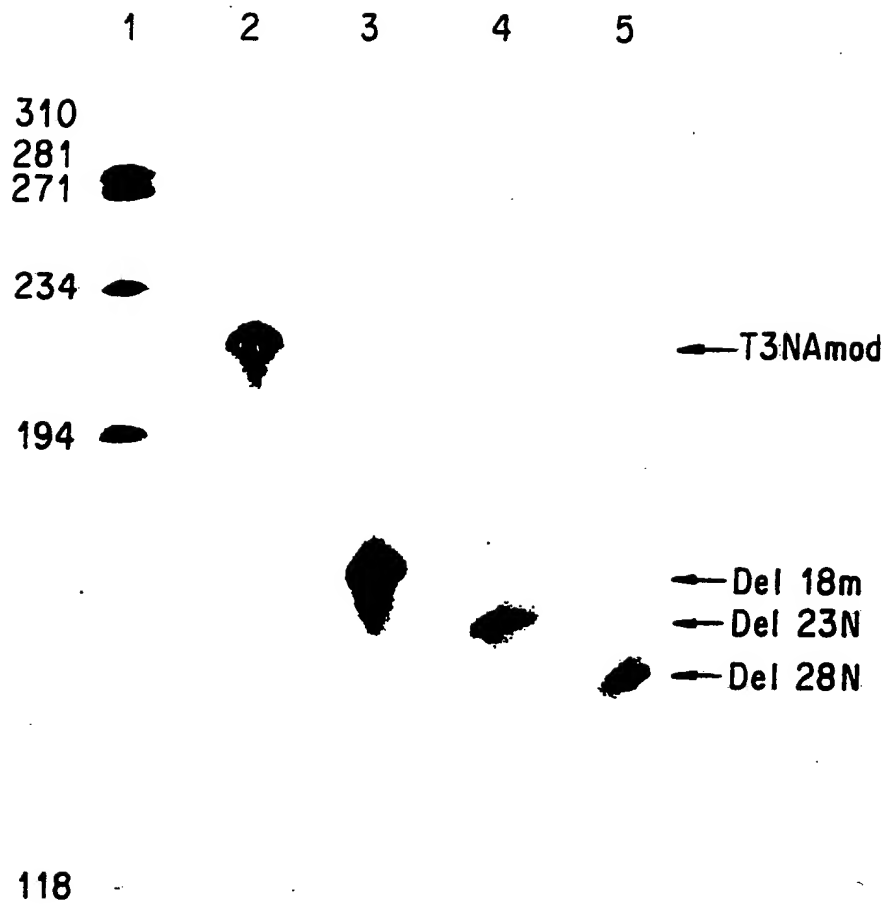


FIG. 10

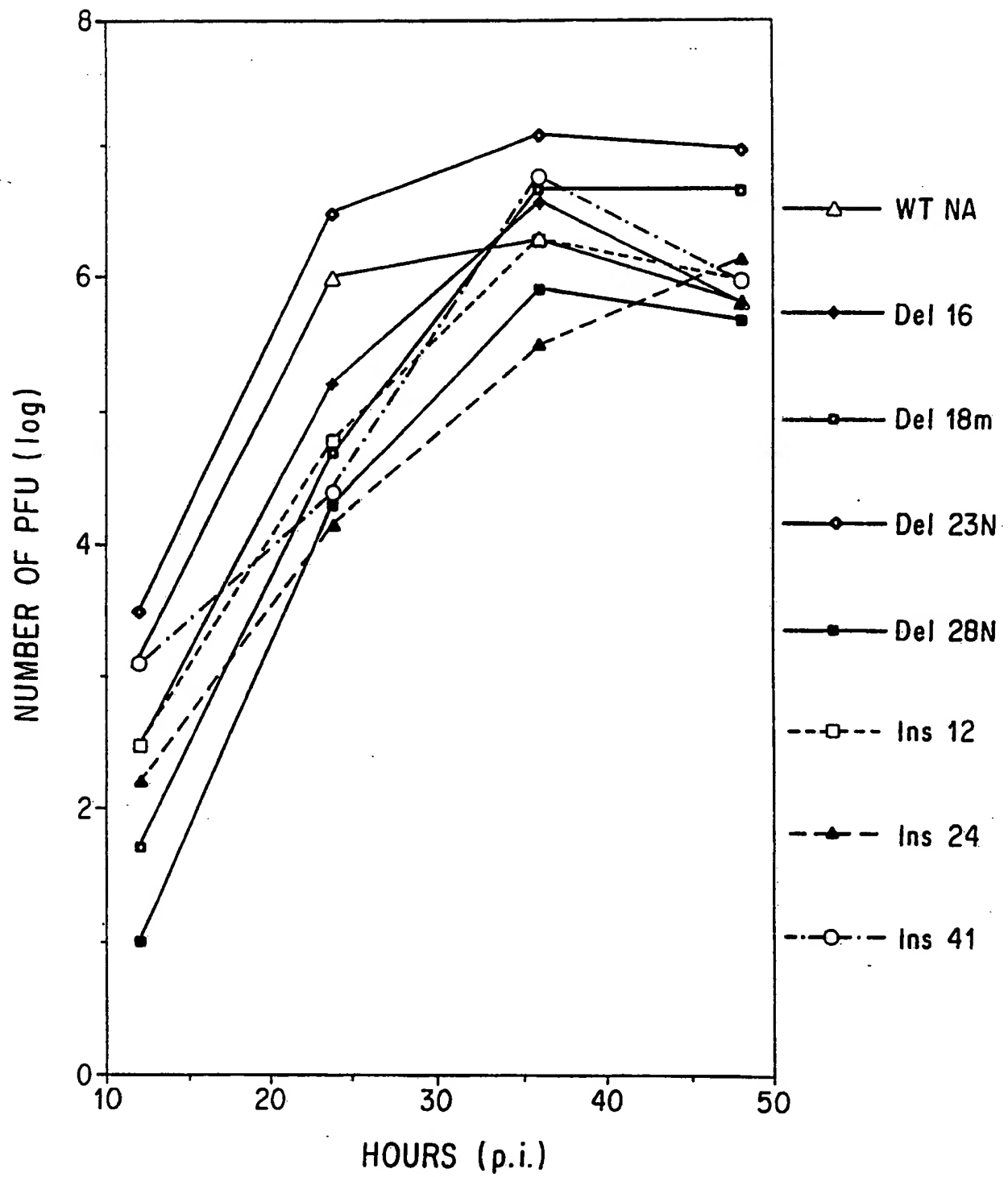


FIG. 11A

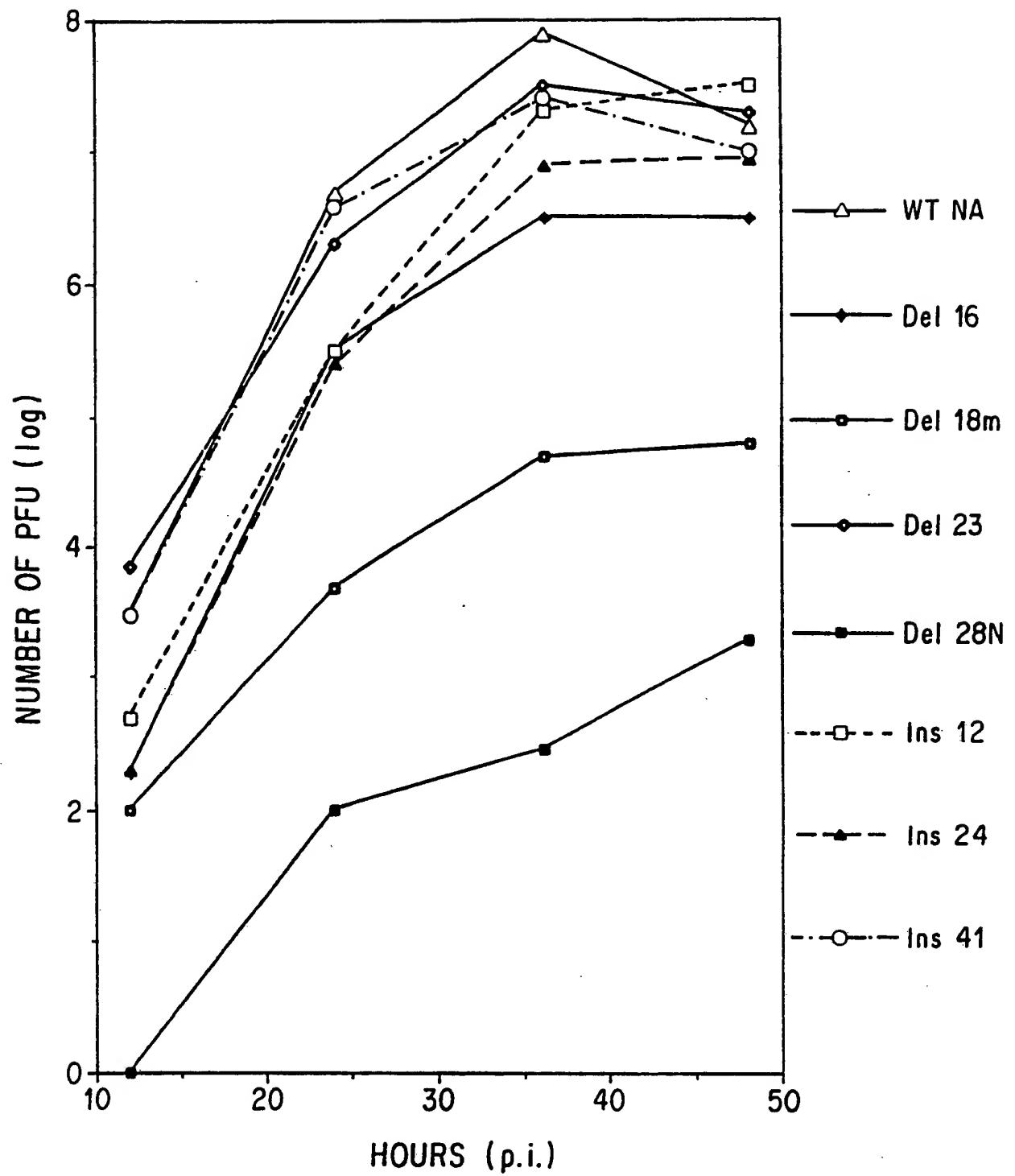


FIG. 11B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/03615

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : Please See Extra Sheet.

US CL : 424/88, 89, 93T; 435/69.3, 172.1, 320.1; 935/32, 47, 57, 65

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/88, 89, 93T; 435/69.3, 172.1, 320.1; 935/32, 47, 57, 65

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, DERWENT, EMBASE, CA, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Virology, Volume 167(2), issued December 1988, N.J. Cox et al, "Identification of Sequence Changes in the Cold-Adapted, Live Attenuated Influenza Vaccine Strain, A/Ann Arbor/6/60(H2N2)", pages 554-567, see Figure 4, Table 1, and page 559.	1 - 3 , 6 , 14 - 17, 20, 27, 36 - 38, 40, 45, 47, 48
X Y	Journal of Virology, Volume 66(1), issued January 1992, A. Li et al, "Influenza A Virus Transfectants with Chimeric Hemagglutinins Containing Epitopes from Different Subtypes", pages 399-404, see abstract and Figure 1.	<u>36-38, 40, 46-48</u> 41-45, 49, 50



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be part of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* & * document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

28 May 1993

Date of mailing of the international search report

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Authorized officer

MICHAEL TUSCAN

Telephone No. (703) 308-0196

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P Y	Journal of Virology, Volume 66(8), issued August 1992, M.R. Castrucci et al, "Attenuation of Influenza A Virus by Insertion of a Foreign Epitope into the Neuraminidase", pages 4647-4653, see abstract and Figure 2.	<u>36-38,40-44,46-50</u> 39,45,51-56
X,P Y	Journal of Virology, Volume 66(8), issued August 1992, G. Luo et al, "Mechanism of Attenuation of a Chimeric Influenza A/B Transfectant Virus", pages 4679-4685, see abstract and Figure 1.	<u>1-3,6,12,15-17,20,25</u> 11,13,14,24,26,27
Y Y	Virology, Volume 175(2), issued April 1990, K.K. Conzelmann et al, "Molecular Cloning and Complete Nucleotide Sequence of the Attenuated Rabies Virus SAD B19", pages 485-499, see entire document.	<u>15,21,23-27,36,39,40,45</u> 22
X	Virology, Volume 173(2), issued December 1989, K. Morimoto et al, "Structure and Transcription of the Glycoprotein Gene of Attenuated HEP-Flury Strain of Rabies Virus", pages 465-477, see entire document, especially the abstract, and Figures 2 and 3.	15,21,23,25,36,39,40
X Y	Journal of Virology, Volume 60(1), issued October 1986, R. Bassel-Duby et al, "Identification of Attenuating Mutations on the Reovirus Type 3 S1 Double-Stranded RNA Segment with a Rapid Sequencing Technique", pages 64-67, see abstract and Table 3.	<u>51-53</u> 7,8,28,29,54-56
X Y	Journal of Virology, Volume 62(11), issued November 1988, K. Nishikawa et al, "Comparative Analysis of the VP3 Gene of Divergent Strains of the Rotaviruses Simian SA-11 and Bovine Nebraska Calf Diarrhea Virus", pages 4022-4026, see entire document, especially p.4023, third paragraph.	<u>51,53</u> 7-10,28-35
X Y	Journal of Virology, Volume 64(6), issued June 1990, M. Philpott et al, "Hemagglutinin Mutations Related to Attenuation and Altered Cell Tropism of a Virulent Avian Influenza A Virus", pages 2941-2947, see Discussion.	<u>36-38,40</u> 1-3,6,12,15-17,20,25
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X Y	Proceedings of the National Academy of Sciences USA, Volume 88, issued June 1991, T. Muster et al, "An Influenza A Virus Containing Influenza B Virus 5' and 3' noncoding regions on the Neuraminidase Gene is Attenuated in Mice", pages 5177-5181, see abstract and Figure 1.	<u>1-3,6,12,15-17,20,25</u> 11,13-14,24,26-27

A. CLASSIFICATION OF SUBJECT MATTER:

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C12N 7/01, 7/04, 15/11, 15/44, 15/45, 15/46, 15/47; A61K 39/12, 39/145, 39/15, 39/155, 39/205